



SEQUENCE LISTING

<110> Kilian, Andrzej
Bowtell, David

<120> VERTEBRATE TELOMERASE GENES AND PROTEINS AND USES
THEREOF

<130> 191106.407C2

<140> 09/502,498

<141> 2000-02-11

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<213> Homo sapiens

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 Phe Leu Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro
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Glu Val Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg
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 Asp Ile His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln
 660 665 670
 Asp Pro Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala
 675 680 685
 Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile
 690 695 700
 Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln
 705 710 715 720
 Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser
 725 730 735
 Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu
 740 745 750
 Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser
 755 760 765
 Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe
 770 775 780
 Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys
 785 790 795 800
 Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu
 805 810 815
 Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp
 820 825 830
 Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His
 835 840 845
 Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro
 850 855 860
 Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro
 865 870 875 880

Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala
 885 890 895
 His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu
 900 905 910
 Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala
 915 920 925
 Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg
 930 935 940
 Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp
 945 950 955 960
 Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile
 965 970 975
 Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro
 980 985 990
 Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile
 995 1000 1005
 Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala
 1010 1015 1020
 Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu
 1025 1030 1035 1040
 Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg
 1045 1050 1055
 His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln
 1060 1065 1070
 Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu
 1075 1080 1085
 Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 1090 1095 1100

<210> 5
 <211> 884
 <212> PRT
 <213> Homo sapiens

<400> 5
 Met Lys Ile Leu Phe Glu Phe Ile Gln Asp Lys Leu Asp Ile Asp Leu
 1 5 10 15

Gln Thr Asn Ser Thr Tyr Lys Glu Asn Leu Lys Cys Gly His Phe Asn

20 25 30
 Gly Leu Asp Glu Ile Leu Thr Thr Cys Phe Ala Leu Pro Asn Ser Arg
 35 40 45
 Lys Ile Ala Leu Pro Cys Leu Pro Gly Asp Leu Ser His Lys Ala Val
 50 55 60
 Ile Asp His Cys Ile Ile Tyr Leu Leu Thr Gly Glu Leu Tyr Asn Asn
 65 70 75 80
 Val Leu Thr Phe Gly Tyr Lys Ile Ala Arg Asn Glu Asp Val Asn Asn
 85 90 95
 Ser Leu Phe Cys His Ser Ala Asn Val Asn Val Thr Leu Leu Lys Gly
 100 105 110
 Ala Ala Trp Lys Met Phe His Ser Leu Val Gly Thr Tyr Ala Phe Val
 115 120 125
 Asp Leu Leu Ile Asn Tyr Thr Val Ile Gln Phe Asn Gly Gln Phe Phe
 130 135 140
 Thr Gln Ile Val Gly Asn Arg Cys Asn Glu Pro His Leu Pro Pro Lys
 145 150 155 160
 Trp Val Gln Arg Ser Ser Ser Ser Ser Ala Thr Ala Ala Gln Ile Lys
 165 170 175
 Gln Leu Thr Glu Pro Val Thr Asn Lys Gln Phe Leu His Lys Leu Asn
 180 185 190
 Ile Asn Ser Ser Ser Phe Phe Pro Tyr Ser Lys Ile Leu Pro Ser Ser
 195 200 205
 Ser Ser Ile Lys Lys Leu Thr Asp Leu Arg Glu Ala Ile Phe Pro Thr
 210 215 220
 Asn Leu Val Lys Ile Pro Gln Arg Leu Lys Val Arg Ile Asn Leu Thr
 225 230 235 240
 Leu Gln Lys Leu Leu Lys Arg His Lys Arg Leu Asn Tyr Val Ser Ile
 245 250 255
 Leu Asn Ser Ile Cys Pro Pro Leu Glu Gly Thr Val Leu Asp Leu Ser
 260 265 270
 His Leu Ser Arg Gln Ser Pro Lys Glu Arg Val Leu Lys Phe Ile Ile
 275 280 285
 Val Ile Leu Gln Lys Leu Leu Pro Gln Glu Met Phe Gly Ser Lys Lys
 290 295 300
 Asn Lys Gly Lys Ile Ile Lys Asn Leu Asn Leu Leu Ser Leu Pro
 305 310 315 320
 Leu Asn Gly Tyr Leu Pro Phe Asp Ser Leu Leu Lys Lys Leu Arg Leu

325 330 335
 Lys Asp Phe Arg Trp Leu Phe Ile Ser Asp Ile Trp Phe Thr Lys His
 340 345 350
 Asn Phe Glu Asn Leu Asn Gln Leu Ala Ile Cys Phe Ile Ser Trp Leu
 355 360 365
 Phe Arg Gln Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr Cys Thr
 370 375 380
 Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe Arg His Asp Thr Trp
 385 390 395 400
 Asn Lys Leu Ile Thr Pro Phe Ile Val Glu Tyr Phe Lys Thr Tyr Leu
 405 410 415
 Val Glu Asn Asn Val Cys Arg Asn His Asn Ser Tyr Thr Leu Ser Asn
 420 425 430
 Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys Lys Ser Asn Asn Glu
 435 440 445
 Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala Asp Glu Glu Glu Phe
 450 455 460
 Thr Ile Tyr Lys Glu Asn His Lys Asn Ala Ile Gln Pro Thr Gln Lys
 465 470 475 480
 Ile Leu Glu Tyr Leu Arg Asn Lys Arg Pro Thr Ser Phe Thr Lys Ile
 485 490 495
 Tyr Ser Pro Thr Gln Ile Ala Asp Arg Ile Lys Glu Phe Lys Gln Arg
 500 505 510
 Leu Leu Lys Lys Phe Asn Asn Val Leu Pro Glu Leu Tyr Phe Met Lys
 515 520 525
 Phe Asp Val Lys Ser Cys Tyr Asp Ser Ile Pro Arg Met Glu Cys Met
 530 535 540
 Arg Ile Leu Lys Asp Ala Leu Lys Asn Glu Asn Gly Phe Phe Val Arg
 545 550 555 560
 Ser Gln Tyr Phe Phe Asn Thr Asn Thr Gly Val Leu Lys Leu Phe Asn
 565 570 575
 Val Val Asn Ala Ser Arg Val Pro Lys Pro Tyr Glu Leu Tyr Ile Asp
 580 585 590
 Asn Val Arg Thr Val His Leu Ser Asn Gln Asp Val Ile Asn Val Val
 595 600 605
 Glu Met Glu Ile Phe Lys Thr Ala Leu Trp Val Glu Asp Lys Cys Tyr
 610 615 620
 Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser Ala Pro Ile

625 630 635 640
 Val Asp Leu Val Tyr Asp Asp Leu Leu Glu Phe Tyr Ser Glu Phe Lys
 645 650 655
 Ala Ser Pro Ser Gln Asp Thr Leu Ile Leu Lys Leu Ala Asp Asp Phe
 660 665 670
 Leu Ile Ile Ser Thr Asp Gln Gln Gln Val Ile Asn Ile Lys Lys Leu
 675 680 685
 Ala Met Gly Gly Phe Gln Lys Tyr Asn Ala Lys Ala Asn Arg Asp Lys
 690 695 700
 Ile Leu Ala Val Ser Ser Gln Ser Asp Asp Thr Val Ile Gln Phe
 705 710 715 720
 Cys Ala Met His Ile Phe Val Lys Glu Leu Glu Val Trp Lys His Ser
 725 730 735
 Ser Thr Met Asn Asn Phe His Ile Arg Ser Lys Ser Ser Lys Gly Ile
 740 745 750
 Phe Arg Ser Leu Ile Ala Leu Phe Asn Thr Arg Ile Ser Tyr Lys Thr
 755 760 765
 Ile Asp Thr Asn Leu Asn Ser Thr Asn Thr Val Leu Met Gln Ile Asp
 770 775 780
 His Val Val Lys Asn Ile Ser Glu Cys Tyr Lys Ser Ala Phe Lys Asp
 785 790 795 800
 Leu Ser Ile Asn Val Thr Gln Asn Met Gln Phe His Ser Phe Leu Gln
 805 810 815
 Arg Ile Ile Glu Met Thr Val Ser Gly Cys Pro Ile Thr Lys Cys Asp
 820 825 830
 Pro Leu Ile Glu Tyr Glu Val Arg Phe Thr Ile Leu Asn Gly Phe Leu
 835 840 845
 Glu Ser Leu Ser Ser Asn Thr Ser Lys Phe Lys Asp Asn Ile Ile Leu
 850 855 860
 Leu Arg Lys Glu Ile Gln His Leu Gln Ala Tyr Ile Tyr Ile Tyr Ile
 865 870 875 880
 His Ile Val Asn

<210> 6
 <211> 13
 <212> DNA
 <213> Homo sapiens
 <220>

<221> intron
 <222> (8)..(13)
 <223> First six bases of Y intron

<400> 6
 ccaggtgggc ctc 13

<210> 7
 <211> 14
 <212> DNA
 <213> Homo sapiens

<220>
 <221> intron
 <222> (1)..(7)
 <223> Last seven bases of intron Y

<400> 7
 gcaggtgtcc tgcc 14

<210> 8
 <211> 14
 <212> DNA
 <213> Homo sapiens

<220>
 <221> intron
 <222> (8)..(14)
 <223> First 7 bases of Intron 1

<400> 8
 aaagagggtg gctg 14

<210> 9
 <211> 14
 <212> DNA
 <213> Homo sapiens

<220>
 <221> intron
 <222> (1)..(7)
 <223> Last 7 bases of Intron 1

<400> 9
 aacagaagcc gagc 14

<210> 10
 <211> 14
 <212> DNA
 <213> Homo sapiens

<220>
 <221> intron
 <222> (8)..(14)
 <223> First 7 bases of Intron Alpha

<400> 10

tgtcaagggtg gatg 14

<210> 11
 <211> 14
 <212> DNA
 <213> Homo sapiens

<220>
 <221> intron
 <222> (1)..(7)
 <223> Last 7 bases of Intron Alpha

<400> 11
 cccccaggac aggc 14

<210> 12
 <211> 14
 <212> DNA
 <213> Homo sapiens

<220>
 <221> intron
 <222> (8)..(14)
 <223> First 7 bases of Intron Beta

<400> 12
 gagccacgtc tcta 14

<210> 13
 <211> 14
 <212> DNA
 <213> Homo sapiens

<220>
 <221> intron
 <222> (1)..(7)
 <223> Last 7 bases of Intron Beta

<400> 13
 ggggcaagtc ctac 14

<210> 14
 <211> 14
 <212> DNA
 <213> Homo sapiens

<220>
 <221> intron
 <222> (8)..(14)
 <223> First 7 base of Intron 2

<400> 14
 actccagggtg agcg 14

<210> 15
 <211> 14
 <212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (1)..(7)

<223> Wherein N is any nucleotide

<220>

<221> intron

<222> (1)..(7)

<223> Last 7 bases of Intron 2

<400> 15

nnnnnnncta tgcc

14

<210> 16

<211> 173

<212> DNA

<213> Homo sapiens

<220>

<221> intron

<222> (8)..(166)

<223> Full Sequence of Intron 3

<400> 16

aacgcagccg aagaaaacat ttctgtcgtg actcctgcgg tgcttgggtc gggacagcca 60
gagatggagc caccgccgag accgtcgggt gtgggcagct ttccggtgtc tcctgggagg 120
ggagttgggc tgggcctgtg actcctcagc ctctgttttc cccagggat gtc 173

<210> 17

<211> 46

<212> PRT

<213> Homo sapiens

<400> 17

Thr Ala Ala Glu Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly
1 5 10 15

Ser Gly Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly
20 25 30

Ser Phe Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu
35 40 45

<210> 18

<211> 104

<212> DNA

<213> Homo sapiens

<220>

<223> Intron Y

<400> 18

ggcctccccg gggtcggcgt ccggctgggg ttgagggcgg ccggggggaa ccagcgacat 60
gcggagagca gcgcaggcga ctcagggcgc ttccccgcga ggtg 104

<210> 19
 <211> 34
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Reding Frame One of Intron Y

<400> 19
 Gly Leu Pro Gly Val Gly Val Arg Leu Gly Leu Arg Ala Ala Gly Gly
 1 5 10 15
 Asn Gln Arg His Ala Glu Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro
 20 25 30

Arg Arg

<210> 20
 <211> 10
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Reading Frame Two of Intron Y before termination
 Codon

<400> 20
 Ala Ser Pro Gly Ser Ala Ser Gly Trp Gly
 1 5 10

<210> 21
 <211> 23
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Reading Frame Two of Intron Y after termination
 Codon

<400> 21
 Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
 1 5 10 15

Gln Gly Ala Ser Pro Ala Gly
 20

<210> 22
 <211> 34
 <212> PRT
 <213> Homo sapiens

<220>

<223> Reading Frame Three of Intron Y

<400> 22

Pro Pro Arg Gly Arg Arg Pro Ala Gly Val Glu Gly Gly Arg Gly Glu
1 5 10 15

Pro Ala Thr Cys Gly Glu Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro
20 25 30

Gln Val

<210> 23

<211> 38

<212> DNA

<213> Homo sapiens

<220>

<223> Intron 1

<400> 23

gtggctgtgc tttggtttta cttccttttt aaccagaa

38

<210> 24

<211> 13

<212> PRT

<213> Homo sapiens

<220>

<223> Intron 1 Translation

<400> 24

Val Ala Val Leu Trp Phe Asn Phe Leu Phe Asn Gln Lys
1 5 10

<210> 25

<211> 36

<212> DNA

<213> Homo sapiens

<220>

<223> Intron Alpha

<400> 25

gtggatgtga cgggcgcgta cgacaccatc cccag

36

<210> 26

<211> 12

<212> PRT

<213> Homo sapiens

<220>

<223> Intron Alpha Translation

<400> 26

Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln
 1 5 10

<210> 27
 <211> 182
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Intron Beta

<400> 27
 gtctctacct tgacagacct ccagccgtac atgcgacagt tcgtggctca cctgcaggag 60
 accagcccgc tgagggatgc cgtcgtcacc gagcagagct cctccctgaa tgaggccagc 120
 agtggcctct tcgacgtctt cctacgcttc atgtgccacc acgccgtgcg catcaggggc 180
 aa 182

<210> 28
 <211> 61
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Intron Beta Translation

<400> 28
 Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala
 1 5 10 15

His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln
 20 25 30

Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu
 35 40 45

Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys
 50 55 60

<210> 29
 <211> 226
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Intron 2

<400> 29
 gtgagcgcac ctggccggaa gtggagcctg tgcccggctg gggcagggtgc tgctgcaggg 60
 ccgttgcgtc cacctctgct tccgtgtggg gcaggcgact gccaatccca aagggtcaga 120
 tgccacaggg tgcccctcgt cccatctggg gctgagcaca aatgcatctt tctgtgggag 180
 tgagggtgcc tcacaacggg agcagttttc tgtgctattt tggtaa 226

<210> 30
 <211> 159
 <212> DNA

<213> Homo sapiens

<220>

<223> Intron 3

<400> 30

```
ccgaagaaaa catttctgtc gtgactcctg cgggtgcttg gtcgggacag ccagagatgg 60
agccaccccg cagaccgtcg ggtgtgggca gctttccggt gtctcctggg aggggagttg 120
ggctgggcct gtgactcctc agcctctgtt ttccccag 159
```

<210> 31

<211> 44

<212> PRT

<213> Homo sapiens

<220>

<223> Intron 3 Translation

<400> 31

```
Ala Glu Glu Asn Ile Ser Val Val Thr Pro Ala Val Leu Gly Ser Gly
  1                      5                      10                      15
```

```
Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe
                20                      25                      30
```

```
Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu
      35                      40
```

<210> 32

<211> 262

<212> DNA

<213> Homo sapiens

<220>

<223> Intron X. Complete length unknown

<400> 32

```
gacagtcacc agggggggttg accgccggac tgggcgtccc caggggttgac tataggacca 60
ggtgtccagg tgccctgcaa gtagaggggc tctcagaggc gtctggctgg catgggtgga 120
cgtggccccc ggcattggcct tctgcgtgtg ctgccgtggg tgccctgagc cctcactgag 180
tcggtggggg cttgtggcct cccgtgagct tccccctagt ctgttgtctg gctgagcaag 240
cctcctgagg ggctctctat tg 262
```

<210> 33

<211> 218

<212> DNA

<213> Homo sapiens

<220>

<223> Partial Sequence of Genomic Intron (approximately 2.7 kb)

<400> 33

```
gtggctgtgc tttggttttaa cttccttttt aaccagaagt gcgtttgagc cccacatttg 60
gtatcagctt agatgaaggg cccggaggag gggccacggg acacagccag ggccatggca 120
cggcgccccc ccatttgtgc gcacagttag gtggccgagg tgccggtgcc tccagaaaag 180
```

cagcgtgggg gtgtaggggg agctcctggg gcagggac

218

<210> 34
<211> 2031
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (1767)..(1769)
<223> Wherein N is A, C, G or T

<220>
<223> N-Terminal Truncated Telomerase

<400> 34

atgcgcgcgc	ctccccgctg	ccgagccgtg	cgctccctgc	tgcgcagcca	ctacfcgcgag	60
gtgctgccgc	tggccacgtt	cgtgcggcgc	ctggggcccc	agggctggcg	gctggtgcag	120
cgcggggacc	cgcgggcttt	ccgcgcgctg	gtggcccagt	gcctggtgtg	cgtgccctgg	180
gacgcacggc	cgccccccgc	cgccccctcc	ttccgccagg	tgtcctgcct	gaaggagctg	240
gtggcccag	tgctgcagag	gctgtgcgag	cgcgggcgca	agaacgtgct	ggccttcggc	300
ttcgcgctgc	tggacggggc	ccgcgggggc	ccccccgagg	ccttcaccac	cagcgtgcgc	360
agctacctgc	ccaacacggt	gaccgacgca	ctgcggggga	gcggggcgctg	ggggctgctg	420
ctgcgcgcgc	tgggcgacga	cgtgctggtt	cacctgctgg	cacgctgcgc	gctctttgtg	480
ctggtggctc	ccagctgcgc	ctaccaggtg	tgcggggcgc	cgctgtacca	gctcggcgct	540
gccactcagg	cccggccccc	gccacacgct	agtggacccc	gaaggcgtct	gggatgcgaa	600
cgggcctgga	accatagcgt	cagggaggcc	ggggctcccc	tgggcctgcc	agccccgggt	660
gcgaggaggc	gcgggggagc	tgccagccga	agtctgccgt	tgcccaagag	gcccaggcgt	720
ggcgtgccc	ctgagccgga	gcggacgccc	gttgggcagg	ggtcctgggc	ccaccggggc	780
aggacgcgtg	gaccgagtga	ccgtgggttt	tgtgtggtgt	cacctgccag	acccgccgaa	840
gaagccacct	ctttggaggg	tgcgtctctt	ggcacgcgcc	actcccaccc	atccgtgggc	900
cgccagcacc	acgcggggcc	cccattccaca	tgcgggccac	cacgtccctg	ggacacgcct	960
tgtcccccg	tgtacgcga	gaccaagcac	ttcctctact	cctcaggcga	caaggagcag	1020
ctgcggccct	ccttcctact	cagctctctg	aggcccagcc	tgactggcgc	tcggaggctc	1080
gtggagacca	tctttctggg	ttccaggccc	tggatgccag	ggactccccg	cagggtgccc	1140
cgctgcccc	agcgtactgt	gcaaattgcgg	ccctgttttc	tggagctgct	tgggaaccac	1200
gcgcagtgcc	cctacggggg	gctcctcaag	acgcactgcc	cgctgcgagc	tgcggtcacc	1260
ccagcagccg	gtgtctgtgc	ccgggagaag	ccccagggct	ctgtggcggc	ccccgaggag	1320
gaggacacag	acccccgtcg	cctggtgcag	ctgctccgcc	agcacagcag	cccctggcag	1380
gtgtacggct	tcgtgcgggc	ctgcctgcgc	cggtggtgc	ccccaggcct	ctggggctcc	1440
aggcacaacg	aacgccgctt	cctcaggaa	accaaagaag	tcattctccct	ggggaagcat	1500
gccaaagctc	cgctgcagga	gctgacgtgg	aagatgagcg	tgcgggactg	cgcttggtcg	1560
cgcaggagcc	caggggttgg	ctgtgttccg	gccgcagagc	accgtctgcg	tgaggagatc	1620
ctggccaagt	tctgcactgt	gctgatgagt	gtgtacgtcg	tcgagctgct	caggctctttc	1680
ttttatgtca	cggagaccac	gtttcaaaag	aaacaggctct	ttttctaccg	gaagagtgtc	1740
tggagcaagt	tgcaaagcat	tgggaatnng	acagtcacca	gggggggtga	ccgccggact	1800
gggcgtcccc	agggttgact	ataggaccag	gtgtccagg	gccctgcaag	tagaggggct	1860
ctcagaggcg	tctggctggc	atgggtggac	gtggcccccg	gcattggcctt	ctgcgtgtgc	1920
tgcctgtggg	gccctgagcc	ctcactgagt	cggtgggggc	ttgtggcttc	ccgtgagctt	1980
ccccctagtc	tgttgtctgg	ctgagcaagg	ctcctgaggg	gctctctatt	g	2031

<210> 35
<211> 588
<212> PRT
<213> Homo sapiens

<220>

<223> Protein Predicted by SEQ ID NO:34

<400> 35

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
 1 18 5 10 15
 His (Thr) Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
 65 70 75 80
 Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
 85 90 95
 Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
 100 105 110
 Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
 115 120 125
 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
 130 135 140
 Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
 145 150 155 160
 Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
 165 170 175
 Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
 180 185 190
 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
 195 200 205
 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
 210 215 220
 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
 225 230 235 240
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
 245 250 255
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
 260 265 270
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285

Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
 500 505 510
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly
 580 585

<210> 36
 <211> 2041
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Truncated Protein 1; Intron 1 Addition

<400> 36
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 cgcggggacc cggcggcttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180
 gacgcacggc cgcgcgcgcg cgcgcctcc ttccgccagg tgcctgcct gaaggagctg 240
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 ctggtggctc ccagctgcgc ctaccagggt tgcgggcgcg cgctgtacca gctcggcgct 540
 gccactcagg cccggccccc gccacacgct agtggacccc gaaggcgtct gggatgcgaa 600
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 aggacgcgtg gaccgagtga ccgtggtttc tgtgtggtgt cacctgccag acccgccgaa 840
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 gtggagacca tctttctggg ttccaggccc tggatgccag ggactcccc caggttgccc 1140
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 a 2041

<210> 37
 <211> 670
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Truncated Protein 1; Encoded by SEQ ID NO:36

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 35 40 45
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
 65 70 75 80
 Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
 85 90 95
 Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
 100 105 110
 Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
 115 120 125
 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
 130 135 140
 Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
 145 150 155 160
 Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
 165 170 175
 Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
 180 185 190
 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
 195 200 205
 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
 210 215 220
 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
 225 230 235 240
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
 245 250 255
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
 260 265 270
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
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 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320

Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
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 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
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 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
 500 505 510
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590
 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620

Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
625 630 635 640

Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Val Ala Val Leu Trp Phe
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Thr Phe Leu Phe Asn Gln Lys Pro Ser Val Ser Phe Arg Gly
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<210> 38
<211> 2541
<212> DNA
<213> Homo sapiens

<220>
<223> Truncated Protein 2; Alpha Intron Addition

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ccccaggaca ggctcacgga ggtcatcgcc agcatcatca aaccacagaa cacgtactgc 2220

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gaagacagtg gtgaacttcc c 2541

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<210> 39
 <211> 806
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Truncated Protein 2; Encoded by SEQ ID NO:38

<400> 39

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Pro	Gln	Gly	Trp	Arg	Leu	Val	Gln	Arg	Gly	Asp	Pro	Ala	Ala	Phe	Arg	35	40	45	
Ala	Leu	Val	Ala	Gln	Cys	Leu	Val	Cys	Val	Pro	Trp	Asp	Ala	Arg	Pro	50	55	60	
Pro	Pro	Ala	Ala	Pro	Ser	Phe	Arg	Gln	Val	Ser	Cys	Leu	Lys	Glu	Leu	65	70	75	80
Val	Ala	Arg	Val	Leu	Gln	Arg	Leu	Cys	Glu	Arg	Gly	Ala	Lys	Asn	Val	85	90	95	
Leu	Ala	Phe	Gly	Phe	Ala	Leu	Leu	Asp	Gly	Ala	Arg	Gly	Gly	Pro	Pro	100	105	110	
Glu	Ala	Phe	Thr	Thr	Ser	Val	Arg	Ser	Tyr	Leu	Pro	Asn	Thr	Val	Thr	115	120	125	
Asp	Ala	Leu	Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu	Leu	Arg	Arg	Val	130	135	140	
Gly	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu	Phe	Val	145	150	155	160
Leu	Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro	Leu	Tyr	165	170	175	
Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala	Ser	Gly	180	185	190	
Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser	Val	Arg	195	200	205	
Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg	Arg	Arg	210	215	220	

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
 225 230 235 240
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
 245 250 255
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
 260 265 270
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
 500 505 510
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525

Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540
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 545 550 555 560
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590
 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700
 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
 705 710 715 720
 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
 725 730 735
 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
 740 745 750
 Gly His Val Arg Lys Ala Phe Lys Ser Val Leu Arg Pro Val Pro Gly
 755 760 765
 Asp Pro Ala Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val Leu
 770 775 780
 Arg Arg His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala Gly Arg Ala
 785 790 795 800
 Ala Pro Ala Phe Val Gly
 805

<211> 3396
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Reference Telomerase; with Intron Alpha and Beta

<400> 40

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<210> 41
<211> 3069
<212> DNA
<213> Homo sapiens

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<220>
<223> Truncated Protein 3; with Introns Alpha, Beta and
2

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ccccaggaca ggctcacgga ggtcatcgcc agcatcatca aaccccagaa cacgtactgc 2220
gtgcgtcggg atgccgtggt ccagaaggcc gcccatgggc acgtccgcaa ggccttcaag 2280

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cagatgccgg cccacggcct attcccctgg tgcggcctgc tgctggatac ccggaccctg 2820
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ttttggtaa 3069

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<210> 42
 <211> 948
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Truncated Protein 3; Encoded by SEQ ID NO:41

<400> 42
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 His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
 65 70 75 80
 Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
 85 90 95
 Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
 100 105 110
 Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
 115 120 125
 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
 130 135 140
 Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
 145 150 155 160
 Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
 165 170 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
 180 185 190
 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
 195 200 205
 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
 210 215 220
 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
 225 230 235 240
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
 245 250 255
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
 260 265 270
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480

Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
 500 505 510
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590
 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700
 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
 705 710 715 720
 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
 725 730 735
 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
 740 745 750
 Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
 755 760 765
 Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
 770 775 780

Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
785 790 795 800

Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
805 810 815

Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
820 825 830

Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
835 840 845

Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
850 855 860

Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
865 870 875 880

Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
885 890 895

Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
900 905 910

Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
915 920 925

Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
930 935 940

Asp Tyr Ser Arg
945

<210> 43
<211> 3362
<212> DNA
<213> Homo sapiens

<220>
<223> Altered C-terminus Protein; with Intron Alpha,
Beta and 3

<400> 43
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cgcggggacc cggcggcttt ccgcgcgctg gtggcccagt gctggtgtg cgtgccctgg 180
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 gtgggcagct ttccggtgct tccctggagg ggagttgggc tgggcctgtg actcctcagc 3300
 ctctgttttc cccagggat gtcgctgggg gccaggggcg ccgcggccc tctgcctcc 3360
 ga 3362

<210> 44

<211> 1096

<212> PRT

<213> Homo sapiens

<220>

<223> Altered C-terminus Protein; Encoded by SEQ ID
NO:43

<400> 44

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His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
 65 70 75 80
 Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
 85 90 95
 Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
 100 105 110
 Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
 115 120 125
 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
 130 135 140
 Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
 145 150 155 160
 Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
 165 170 175
 Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
 180 185 190
 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
 195 200 205
 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
 210 215 220
 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
 225 230 235 240
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
 245 250 255
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
 260 265 270
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320

Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
 500 505 510
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590
 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620

Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700
 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
 705 710 715 720
 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
 725 730 735
 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
 740 745 750
 Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
 755 760 765
 Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
 770 775 780
 Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
 785 790 795 800
 Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
 805 810 815
 Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
 820 825 830
 Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
 835 840 845
 Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
 850 855 860
 Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
 865 870 875 880
 Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
 885 890 895
 Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
 900 905 910
 Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
 915 920 925

Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
930 935 940

Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe
945 950 955 960

Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly
965 970 975

Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn
980 985 990

Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln
995 1000 1005

Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln
1010 1015 1020

Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala
1025 1030 1035 1040

Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu Glu Asn
1045 1050 1055

Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro Glu Met
1060 1065 1070

Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe Pro Val Ser Pro
1075 1080 1085

Gly Arg Gly Val Gly Leu Gly Leu
1090 1095

<210> 45
<211> 3918
<212> DNA
<213> Homo sapiens

<220>
<223> Protein that lacks Motif A; with Intron Beta

<400> 45
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cgcggggacc cggcggttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180
gacgcacggc cgccccccgc cgccccctcc ttccgccagg tgcctgcct gaaggagctg 240
gtggcccagag tgctgcagag gctgtgcgag cgcggcgcca agaactgct ggccttcggc 300
ttcgcgctgc tggacggggc ccgcgggggc cccccgagg ccttcaccac cagcgtgcgc 360
agctacctgc ccaacacggt gaccgacgca ctgcggggga gcggggcgctg ggggctgctg 420
ctgcgcgcgc tgggcgacga cgtgctggtt cacctgctgg cacgctgcgc gctctttgtg 480
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TAC

||

tyrosine

||

Y

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<210> 46
 <211> 1120
 <212> PRT

<213> Homo sapiens

<220>

<223> Protein that lacks Motif A; Encoded by SEQ ID
NO:45

<400> 46

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His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
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Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
65 70 75 80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
85 90 95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
100 105 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
115 120 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
130 135 140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
145 150 155 160

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
165 170 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
180 185 190

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
195 200 205

Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
210 215 220

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
225 230 235 240

Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
245 250 255

Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
260 265 270

Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 Val Arg Ala Cys Leu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 465 470 475 480
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
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 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540
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 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575

Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
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 595 600 605
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
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 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700
 Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala Ser Ile
 705 710 715 720
 Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln
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 Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser
 740 745 750
 Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu
 755 760 765
 Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser
 770 775 780
 Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe
 785 790 795 800
 Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys
 805 810 815
 Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu
 820 825 830
 Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp
 835 840 845
 Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His
 850 855 860
 Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro
 865 870 875 880

Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro
 885 890 895
 Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala
 900 905 910
 His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu
 915 920 925
 Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala
 930 935 940
 Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg
 945 950 955 960
 Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp
 965 970 975
 Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile
 980 985 990
 Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro
 995 1000 1005
 Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile
 1010 1015 1020
 Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala
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 Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu
 1045 1050 1055
 Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg
 1060 1065 1070
 His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln
 1075 1080 1085
 Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu
 1090 1095 1100
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<210> 47
 <211> 3033
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Truncated Protein that lacks Motif A; with Introns

Beta and 2

<400> 47

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<210> 48

<211> 936

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein that lacks Motif A; Encoded by
SEQ ID NO:47

<400> 48

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35 40 45
Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60
Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
65 70 75 80
Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
85 90 95
Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
100 105 110
Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
115 120 125
Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
130 135 140
Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
145 150 155 160
Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
165 170 175
Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
180 185 190
Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
195 200 205
Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
210 215 220
Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
225 230 235 240
Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
245 250 255
Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val

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Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp	Thr	Pro
		305			310					315					
Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser	Ser	Gly
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Arg	Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu	Pro	Gln
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			420					425							
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		465			470										
Arg	His	Asn	Glu	Arg	Arg	Phe	Leu	Arg	Asn	Thr	Lys	Lys	Phe	Ile	Ser
				485					490						
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Ser	Val	Arg	Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val	Gly	Cys
		515					520								
Val	Pro	Ala	Ala	Glu	His	Arg	Leu	Arg	Glu	Glu	Ile	Leu	Ala	Lys	Phe
		530				535									
Leu	His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg	Ser	Phe
		545			550										
Phe	Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe	Phe	Tyr

565					570					575					
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Leu	Lys	Arg	Val	Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu	Val	Arg	Gln
		595					600					605			
His	Arg	Glu	Ala	Arg	Pro	Ala	Leu	Leu	Thr	Ser	Arg	Leu	Arg	Phe	Ile
	610					615					620				
Pro	Lys	Pro	Asp	Gly	Leu	Arg	Pro	Ile	Val	Asn	Met	Asp	Tyr	Val	Val
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Gly	Ala	Arg	Thr	Phe	Arg	Arg	Glu	Lys	Arg	Ala	Glu	Arg	Leu	Thr	Ser
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			660					665					670		
Pro	Gly	Leu	Leu	Gly	Ala	Ser	Val	Leu	Gly	Leu	Asp	Asp	Ile	His	Arg
		675					680					685			
Ala	Trp	Arg	Thr	Phe	Val	Leu	Arg	Val	Arg	Ala	Gln	Asp	Pro	Pro	Pro
	690					695					700				
Glu	Leu	Tyr	Phe	Val	Lys	Asp	Arg	Leu	Thr	Glu	Val	Ile	Ala	Ser	Ile
	705					710					715				720
Ile	Lys	Pro	Gln	Asn	Thr	Tyr	Cys	Val	Arg	Arg	Tyr	Ala	Val	Val	Gln
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Lys	Ala	Ala	His	Gly	His	Val	Arg	Lys	Ala	Phe	Lys	Ser	His	Val	Ser
			740					745					750		
Thr	Leu	Thr	Asp	Leu	Gln	Pro	Tyr	Met	Arg	Gln	Phe	Val	Ala	His	Leu
		755					760					765			
Gln	Glu	Thr	Ser	Pro	Leu	Arg	Asp	Ala	Val	Val	Ile	Glu	Gln	Ser	Ser
	770					775					780				
Ser	Leu	Asn	Glu	Ala	Ser	Ser	Gly	Leu	Phe	Asp	Val	Phe	Leu	Arg	Phe
	785					790					795			800	
Met	Cys	His	His	Ala	Val	Arg	Ile	Arg	Gly	Lys	Ser	Tyr	Val	Gln	Cys
				805					810					815	
Gln	Gly	Ile	Pro	Gln	Gly	Ser	Ile	Leu	Ser	Thr	Leu	Leu	Cys	Ser	Leu
			820					825					830		
Cys	Tyr	Gly	Asp	Met	Glu	Asn	Lys	Leu	Phe	Ala	Gly	Ile	Arg	Arg	Asp
		835					840					845			
Gly	Leu	Leu	Leu	Arg	Leu	Val	Asp	Asp	Phe	Leu	Leu	Val	Thr	Pro	His
	850					855					860				
Leu	Thr	His	Ala	Lys	Thr	Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly	Val	Pro

ggagccagaa cgttccgcag agaaaagagg gccgagcgtc tcacctcgag ggtgaaggca 1980
 ctgttcagcg tgctcaacta cgagcgggcg cggcgccccg gcctcctggg cgctctgtg 2040
 ctgggcctgg acgatatcca cagggcctgg cgcaccttcg tgctgcgtgt gcgggcccag 2100
 gaccgcgcgc ctgagctgta ctttgtcaag gacaggctca cggaggtcat cgccagcatc 2160
 atcaaaccac agaacacgta ctgcgtgcgt cggatgcccg tgggccagaa ggccgcccac 2220
 gggcacgtcc gcaaggcctt caagagccac gtctctacct tgacagacct ccagccgtac 2280
 atgcgacagt tcgtggctca cctgcaggag accagcccgc tgagggatgc cgtcgtcatc 2340
 gagcagagct cctccctgaa tgaggccagc agtggcctct tcgacgtctt cctacgcttc 2400
 atgtgccacc acgcgctgcg catcaggggc aagtcctacg tccagtgccg ggggatcccg 2460
 cagggctcca tcctctccac gctgctctgc agcctgtgct acggcgacat ggagaacaag 2520
 ctgtttgcgg ggattcggcg ggacgggctg ctctgcgtt tgggtgatga tttcttggtg 2580
 gtgacacctc acctaccca cgcgaaaacc ttctcagga ccctgggccg aggtgtccct 2640
 gagtatggct gcgtggtgaa cttgcggaag acagtggatg acttccctgt agaagacgag 2700
 gccctgggtg gcacggcttt tgttcagatg cgggcccacg gcctattccc ctgggtgcggc 2760
 ctgctgctgg ataccggac cctggagggtg cagagcgact actccagcta tgcccggacc 2820
 tccatcagag ccagtctcac cttcaaccgc ggcttcaagg ctgggaggaa catgcgtcgc 2880
 aaactctttg gggctcttgcg gctgaagtgt cacagcctgt ttctggattt gcaggtgaac 2940
 agcctccaga cgggtgtgcac caacatctac aagatcctcc tgctgcaggc gtacaggttt 3000
 cacgcatgtg tgctgcagct cccatttcat cagcaagttt ggaagaaccc cacatttttc 3060
 ctgcgcgtca tctctgacac ggcctccctc tgctactcca tcctgaaagc caagaacgca 3120
 gccgaagaaa acattttctgt cgtgactcct gcggtgcttg ggtcgggaca gccagagatg 3180
 gagccacccc gcagaccgtc ggggtgtggc agctttccgg tgtctcctgg gaggggagtt 3240
 gggctggggc tgtgactcct cagcctctgt tttccccag ggatgtcgtt gggggccaag 3300
 ggcgcgcgcg gccctctgac ctccga 3326

<210> 50
 <211> 1084
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Protein Lacking Motif A and Altered C-Terminus;
 Encoded by SEQ ID NO:49

<400> 50
 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
 1 5 10 15
 His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
 65 70 75 80
 Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
 85 90 95
 Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
 100 105 110
 Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr

115 120 125
 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
 130 135 140
 Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
 145 150 155 160
 Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
 165 170 175
 Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
 180 185 190
 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
 195 200 205
 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
 210 215 220
 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
 225 230 235 240
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
 245 250 255
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
 260 265 270
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln

✓

725 730 735
 Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser
 740 745 750
 Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu
 755 760 765
 Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser
 770 775 780
 Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe
 785 790 795 800
 Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys
 805 810 815
 Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu
 820 825 830
 Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp
 835 840 845
 Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His
 850 855 860
 Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro
 865 870 875 880
 Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro
 885 890 895
 Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala
 900 905 910
 His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu
 915 920 925
 Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala
 930 935 940
 Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg
 945 950 955 960
 Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp
 965 970 975
 Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile
 980 985 990
 Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro
 995 1000 1005
 Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile
 1010 1015 1020
 Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala

1025 1030 1035 1040
 Glu Glu Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly
 1045 1050 1055
 Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe
 1060 1065 1070
 Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu
 1075 1080

<210> 51
 <211> 2135
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (1871)..(1873)
 <223> Wherein N is A, C, G or T

<220>
 <223> N-Terminal Truncated Telomerase (ver. 2); with
 Intron Y

<400> 51
 atgccgcgcg ctccccgctg ccgagccgtg cgtccctgc tgcgcagcca ctaccgcgag 60
 gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctgggtgcag 120
 cgcggggacc cggcggtttt ccgcgcgctg gtggcccagt gcctgggtgtg cgtgcccttg 180
 gacgcacggc cggccccccg cggccccctc ttccgccagg tgggcctccc cggggtcggc 240
 gtcgggtgtg ggttgagggc ggccgggggg aaccagcgac atgcggagag cagcgcaggc 300
 gactcagggc gcttcccccg caggtgtcct gcctgaagga gctgggtggc cgagtgtgc 360
 agaggctgtg cgagcgcggc gcgaagaacg tgcctggcctt cggttcgcg ctgctggacg 420
 gggcccgcg gggccccccc gaggccttca ccaccagcgt gcgcagctac ctgcccaca 480
 cgggtgaccga cgcactgcgg gggagcgggg cgtgggggct gctgctgcgc cgcgtgggcg 540
 acgacgtgct ggttcacctg ctggcacgct gcgcgctctt tgtgctggtg gctcccagct 600
 gcgcctacca ggtgtgcggg ccgcgcgtgt accagctcgg cgtgccact caggccccgc 660
 ccccgccaca cgtagtggg ccccggaagg gtctgggatg cgaacgggccc tggaaaccata 720
 gcgtcagggg ggccgggggt cccctgggccc tgccagcccc ggggtgcgag aggcgcgggg 780
 gcagtgccag ccgaagtctg ccgttgccca agaggcccag gcgtggcgct gccctgagc 840
 cggagcggac gcccgttggg caggggtcct gggcccaccc gggcaggacg cgtggaccga 900
 gtgaccgtgg tttctgtgtg gtgtcacctg ccagaccgcg cgaagaagcc acctctttgg 960
 aggggtgcgt ctctggcacg cgcactccc acccatcgt gggccgcccag caccacgcgg 1020
 gccccccatc cacatcgcg ccaccacgtc cctgggacac gccttgtccc ccggtgtacg 1080
 ccgagaccaa gcaattcctc tactcctcag gcgacaagga gcagctgcgg cctccttcc 1140
 tactcagctc tctgaggccc agcctgactg gcgctcggag gctcgtggag accatctttc 1200
 tgggttccag gccctggatg ccagggaact cccgcagggt gccccgcctg cccagcgt 1260
 actggcaaat gcggccccctg tttctggagc tgcttgggaa ccacgcgcag tgccccacg 1320
 ggggtgctcct caagacgcac tgcccgtgc gagctgcgt caccacagca gccggtgtct 1380
 gtgcccggga gaagccccag ggctctgtgg cggccccga ggaggaggac acagaccccc 1440
 gtcgcctggt gcagctgtc cgcacgcaca gcagcccctg gcaggtgtac ggcttcgtgc 1500
 gggcctgct gcgcgggctg gtgccccag gcctctgggg ctccaggcac aacgaacgcc 1560
 gcttctcag gaacaccaag aagttcatct ccctggggaa gcatgccaag ctctcgctgc 1620
 aggagctgac gtggaagatg agcgtgcggg actgcgctt gctgcgcagg agcccagggg 1680
 ttggctgtgt tccggccgca gagcaccgtc tgcgtgagga gatcctggcc aagttcctgc 1740
 actggctgat gagtgtgtac gtcgtcgagc tgctcagggt tttcttttat gtcacggaga 1800

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ccacgtttca aaagaacagg ctctttttct accggaagag tgtctggagc aagttgcaaa 1860
gcattggaat nnnacagtc accagggggg ttgaccgccg gactgggcgt cccaggggtt 1920
gactatagga ccaggtgtcc aggtgccctg caagtagagg ggctctcaga ggcgtctggc 1980
tggcatgggt ggacgtggcc ccgggcatgg ccttctgcgt gtgctgccgt gggtgccctg 2040
agccctcact gagtcggtgg gggcttgtgg cttcccgtga gcttccccct agtctgttgt 2100
ctggctgagc aagcctcctg aggggctctc tattg 2135

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<210> 52
 <211> 622
 <212> PRT
 <213> Homo sapiens

<220>
 <223> N-Terminal Truncated Telomerase (ver.2); encoded
 by SEQ ID NO:51 and ORF1 of Intron Y

<400> 52
 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
 1 5 10 15
 His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
 65 70 75 80
 Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
 85 90 95
 Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
 100 105 110
 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
 115 120 125
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
 130 135 140
 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
 145 150 155 160
 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
 165 170 175
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
 180 185 190
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
 195 200 205
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala

210	215	220
Ser Gly Pro Arg Arg Arg	Leu Gly Cys Glu Arg	Ala Trp Asn His Ser
225	230	235 240
Val Arg Glu Ala Gly	Val Pro Leu Gly	Leu Pro Ala Pro Gly
	245	250 255
Arg Arg Gly Gly Ser Ala Ser Arg Ser	Leu Pro Leu Pro	Lys Arg Pro
	260	265 270
Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro	Val Gly Gln Gly	
	275	280 285
Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe		
	290	295 300
Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu		
305	310	315 320
Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln		
	325	330 335
His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp		
	340	345 350
Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser		
	355	360 365
Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu		
	370	375 380
Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu		
385	390	395 400
Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu		
	405	410 415
Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly		
	420	425 430
Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro		
	435	440 445
Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys		
	450	455 460
Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg		
465	470	475 480
Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr		
	485	490 495
Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp		
	500	505 510
Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe		

515					520					525					
Ile	Ser	Leu	Gly	Lys	His	Ala	Lys	Leu	Ser	Leu	Gln	Glu	Leu	Thr	Trp
530						535					540				
Lys	Met	Ser	Val	Arg	Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val
545					550					555					560
Gly	Cys	Val	Pro	Ala	Ala	Glu	His	Arg	Leu	Arg	Glu	Glu	Ile	Leu	Ala
				565					570					575	
Lys	Phe	Leu	His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg
			580					585					590		
Ser	Phe	Phe	Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe
			595				600					605			
Phe	Tyr	Arg	Lys	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly		
610					615					620					

<210> 53
 <211> 84
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Splicing Variant of Human Telomerase encoded by
 Intron Y, ORF2, before the termination codon.
 SEQ ID NOs: 51,55,59,63,67,71,75,79,83 encode this
 fragment

<400> 53															
Met	Pro	Arg	Ala	Pro	Arg	Cys	Arg	Ala	Val	Arg	Ser	Leu	Leu	Arg	Ser
1				5					10					15	
His	Thr	Arg	Glu	Val	Leu	Pro	Leu	Ala	Thr	Phe	Val	Arg	Arg	Leu	Gly
			20					25					30		
Pro	Gln	Gly	Trp	Arg	Leu	Val	Gln	Arg	Gly	Asp	Pro	Ala	Ala	Phe	Arg
		35					40					45			
Ala	Leu	Val	Ala	Gln	Cys	Leu	Val	Cys	Val	Pro	Trp	Asp	Ala	Arg	Pro
	50					55					60				
Pro	Pro	Ala	Ala	Pro	Ser	Phe	Arg	Gln	Val	Ala	Ser	Pro	Gly	Ser	Ala
65					70					75					80
Ser Gly Trp Gly															

<210> 54
 <211> 537
 <212> PRT
 <213> Homo sapiens

<220>

<223> N-Terminal Truncated Telomerase (ver. 2); encoded
by SEQ ID NO:51, with Y intron, ORF2, after the
termination codon

<400> 54

Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
1 5 10 15

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg
20 25 30

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg
130 135 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
145 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser
165 170 175

Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala
180 185 190

Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
195 200 205

Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro
210 215 220

Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly
225 230 235 240

Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro
245 250 255

Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro
260 265 270

Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu
 275 280 285
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr
 290 295 300
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp
 305 310 315 320
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp
 325 330 335
 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys
 340 345 350
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val
 355 360 365
 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val
 370 375 380
 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu
 385 390 395 400
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala
 405 410 415
 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
 420 425 430
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
 435 440 445
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
 450 455 460
 Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
 465 470 475 480
 Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
 485 490 495
 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
 500 505 510
 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
 515 520 525
 Val Trp Ser Lys Leu Gln Ser Ile Gly
 530 535

<210> 55
 <211> 2145
 <212> DNA
 <213> Homo sapiens

<220>

<223> Truncated Protein 1 (ver.2); with Introns Y and 1

<400> 55

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atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctgggtgcag 120
cgcgggggacc cggcgggttt ccgcgcgctg gtggcccagt gcctgggtgtg cgtgccctgg 180
gacgcacggc cgcggggggc cgcggggggc ttccggcagg tgggcctccc cggggtcggc 240
gtccggctgg gggttagggc ggccgggggg aaccagcgac atgcggagag cagcgcaggc 300
gactcagggc gcttcccccg caggtgtcct gcctgaagga gctgggtggc cgagtgtctc 360
agaggctgtg cgagcgcggc gcgaagaacg tctggcctt cggcttcgcg ctgtgtgacg 420
gggcccgcgg gggccccccc gaggccttca ccaccagcgt gcgcagctac ctgccaaca 480
cgggtgaccga cgcactgcgg gggagcgggg cgtgggggct gctgtctgcg cgcgtggcg 540
acgacgtgct gggtcacctg ctggcacgct gcgcgtctt tgtgtgtgtg gctcccagct 600
gcgcctacca ggtgtgcggg ccgcgcgtgt accagctcgg cgtgccact caggcccggc 660
ccccgccaca cgctagtggc cccgaaggc gtctgggatg cgaacgggcc tggaccata 720
gcgtcaggga ggccgggggt cccctgggccc tggcagcccc ggggtgcgag aggcgcggg 780
gcagtgccag ccgaagtctg ccgttgccca agaggccag gcgtggcgct gcccctgagc 840
cggagcggac gcccggtggg caggggtcct gggccacccc gggcaggacg cgtggaccga 900
gtgaccgtgg tttctgtgtg gtgtcacctg ccagaccgcg cgaagaagcc acctctttgg 960
aggggtgcgt ctctggcacg cgcactccc acccatccgt gggccgccag caccacgcgg 1020
gccccccatc cacatcgcgg ccaccacgtc cctgggacac gccttgtccc ccggtgtacg 1080
ccgagaccaa gcaattcctc tactcctcag gcgacaagga gcagctgcgg cctccttccc 1140
tactcagctc tctgaggccc agcctgactg gcgctcggag gctcgtggag accatcttcc 1200
tgggttccag gccctggatg ccagggactc cccgcagggt gcccgcctg cccagcgt 1260
actggcaaat gcggcccctg tttctggagc tgcctgggaa ccacgcgcag tgcccctacg 1320
gggtgtcct caagacgcac tgcgcgtgc gagctgcggt cccccagca gccggtgtct 1380
gtgcccggga gaagccccag ggctctgtgg cggccccga ggaggaggac acagaccccc 1440
gtcgcttgt gcagctgtc cgcagcaca gcagccctg gcaggtgtac ggcttcgtgc 1500
gggcctgct gcgcgggctg gtgccccag gcctctgggg ctccaggcac aacgaacgcc 1560
gcttctcag gaacaccaag aagttcatct ccctggggaa gcatgccaag ctctcgtctc 1620
aggagctgac gtggaagatg agcgtgcggg actgcgcttg gctgcgcagg agcccagggg 1680
ttgctgtgt tccggccgca gagcacgctc tgcgtgagga gatcctggcc aagttcctgc 1740
actggctgat gagtgtgtac gtcgtcagc tgcctaggctc tttcttttat gtcacggaga 1800
ccacgtttca aaagaacagg ctctttttct accggaagag tgtctggagc aagttgcaaa 1860
gcattggaat cagacagcac ttgaagaggg tgcagctgcg ggagctgtcg gaagcagagg 1920
tcaggcagca tcgggaagcc aggccgccc tgcgtacgtc cagactccgc ttcaccccca 1980
agcctgacgg gctgcggcgg attgtgaaca tggactacgt cgtgggagcc agaacgttcc 2040
gcagagaaaa gaggggtggc gtgctttggg ttaacttctc ttttaaccag aagccgagcg 2100
tctcacctcg aggggtgaagg cactgttcag cgtgctcaac tacga 2145

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<210> 56

<211> 704

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein 1 (ver.2); encoded by SEQ ID
NO:55, with Y Intron ORF1

<400> 56

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Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
  1             5             10             15

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His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
      20             25             30

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Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
 65 70 75 80
 Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
 85 90 95
 Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
 100 105 110
 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
 115 120 125
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
 130 135 140
 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
 145 150 155 160
 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
 165 170 175
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
 180 185 190
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
 195 200 205
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
 210 215 220
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
 225 230 235 240
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
 245 250 255
 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
 260 265 270
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 275 280 285
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
 290 295 300
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 305 310 315 320
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 325 330 335

His	His	Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp	
			340					345					350			
Thr	Pro	Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser	
		355					360					365				
Ser	Gly	Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu	
	370					375					380					
Arg	Pro	Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu	
385					390					395					400	
Gly	Ser	Arg	Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu	
				405					410					415		
Pro	Gln	Arg	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly	
			420					425					430			
Asn	His	Ala	Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro	
		435					440					445				
Leu	Arg	Ala	Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys	
	450					455					460					
Pro	Gln	Gly	Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg	
465					470					475					480	
Arg	Leu	Val	Gln	Leu	Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	Tyr	
			485						490					495		
Gly	Phe	Val	Arg	Ala	Cys	Leu	Arg	Arg	Leu	Val	Pro	Pro	Gly	Leu	Trp	
			500					505					510			
Gly	Ser	Arg	His	Asn	Glu	Arg	Arg	Phe	Leu	Arg	Asn	Thr	Lys	Lys	Phe	
		515					520					525				
Ile	Ser	Leu	Gly	Lys	His	Ala	Lys	Leu	Ser	Leu	Gln	Glu	Leu	Thr	Trp	
	530					535					540					
Lys	Met	Ser	Val	Arg	Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val	
545					550					555					560	
Gly	Cys	Val	Pro	Ala	Ala	Glu	His	Arg	Leu	Arg	Glu	Glu	Ile	Leu	Ala	
				565					570					575		
Lys	Phe	Leu	His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg	
			580					585					590			
Ser	Phe	Phe	Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe	
		595					600					605				
Phe	Tyr	Arg	Lys	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile	Arg	
	610					615					620					
Gln	His	Leu	Lys	Arg	Val	Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu	Val	
625					630					635					640	

Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
645 650 655
Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
660 665 670
Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Val Ala Val Leu
675 680 685
Trp Phe Thr Phe Leu Phe Asn Gln Lys Pro Ser Val Ser Phe Arg Gly
690 695 700

<210> 57
<211> 619
<212> PRT
<213> Homo sapiens

<220>
<223> Truncated Protein 1 (ver.2): encoded by SEQ ID
NO:55, with Intron Y ORF2 after the termination
codon

<400> 57
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Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg
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Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
35 40 45
Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
50 55 60
Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
65 70 75 80
Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
85 90 95
Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
100 105 110
Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
115 120 125
Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg
130 135 140
Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
145 150 155 160

Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg	Arg	Arg	Gly	Gly	Ser		
				165					170					175			
Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro	Arg	Arg	Gly	Ala	Ala		
			180					185					190				
Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly	Ser	Trp	Ala	His	Pro		
		195					200					205					
Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe	Cys	Val	Val	Ser	Pro		
	210					215					220						
Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu	Gly	Ala	Leu	Ser	Gly		
225					230					235					240		
Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln	His	His	Ala	Gly	Pro		
				245					250					255			
Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp	Thr	Pro	Cys	Pro	Pro		
			260					265					270				
Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser	Ser	Gly	Asp	Lys	Glu		
		275					280					285					
Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu	Arg	Pro	Ser	Leu	Thr		
	290					295					300						
Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu	Gly	Ser	Arg	Pro	Trp		
305					310					315					320		
Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu	Pro	Gln	Arg	Tyr	Trp		
				325					330					335			
Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly	Asn	His	Ala	Gln	Cys		
			340					345					350				
Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro	Leu	Arg	Ala	Ala	Val		
		355					360					365					
Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys	Pro	Gln	Gly	Ser	Val		
	370					375					380						
Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg	Arg	Leu	Val	Gln	Leu		
385					390					395					400		
Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	Tyr	Gly	Phe	Val	Arg	Ala		
				405					410					415			
Cys	Leu	Arg	Arg	Leu	Val	Pro	Pro	Gly	Leu	Trp	Gly	Ser	Arg	His	Asn		
				420				425					430				
Glu	Arg	Arg	Phe	Leu	Arg	Asn	Thr	Lys	Lys	Phe	Ile	Ser	Leu	Gly	Lys		
		435					440					445					
His	Ala	Lys	Leu	Ser	Leu	Gln	Glu	Leu	Thr	Trp	Lys	Met	Ser	Val	Arg		
	450					455					460						

Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
 465 470 475 480
 Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
 485 490 495
 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
 500 505 510
 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
 515 520 525
 Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg
 530 535 540
 Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu
 545 550 555 560
 Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
 565 570 575
 Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg
 580 585 590
 Thr Phe Arg Arg Glu Lys Arg Val Ala Val Leu Trp Phe Thr Phe Leu
 595 600 605
 Phe Asn Gln Lys Pro Ser Val Ser Phe Arg Gly
 610 615

<210> 58
 <211> 704
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Truncated Protein 1 (ver.2); encoded by SEQ ID
 NO:55, with Intron Y ORF3

<400> 58
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 His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
 65 70 75 80
 Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu

85					90					95					
Gln	Arg	Arg	Arg	Leu	Arg	Ala	Leu	Pro	Pro	Gln	Val	Ser	Cys	Leu	Lys
			100					105					110		
Glu	Leu	Val	Ala	Arg	Val	Leu	Gln	Arg	Leu	Cys	Glu	Arg	Gly	Ala	Lys
		115					120					125			
Asn	Val	Leu	Ala	Phe	Gly	Phe	Ala	Leu	Leu	Asp	Gly	Ala	Arg	Gly	Gly
	130					135					140				
Pro	Pro	Glu	Ala	Phe	Thr	Thr	Ser	Val	Arg	Ser	Tyr	Leu	Pro	Asn	Thr
	145					150					155				160
Val	Thr	Asp	Ala	Leu	Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu	Leu	Arg
				165					170						175
Arg	Val	Gly	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu
			180					185					190		
Phe	Val	Leu	Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro
		195					200					205			
Leu	Tyr	Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala
	210					215					220				
Ser	Gly	Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser
	225					230					235				240
Val	Arg	Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg
				245					250					255	
Arg	Arg	Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro
			260					265					270		
Arg	Arg	Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly
			275				280					285			
Ser	Trp	Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe
	290					295					300				
Cys	Val	Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu
	305					310					315				320
Gly	Ala	Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln
				325					330					335	
His	His	Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp
			340					345					350		
Thr	Pro	Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser
		355					360					365			
Ser	Gly	Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu
	370					375					380				
Arg	Pro	Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu

385		390		395		400
Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu						
		405		410		415
Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly						
		420		425		430
Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro						
		435		440		445
Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys						
		450		455		460
Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg						
		465		470		475
Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr						
		485		490		495
Gly Phe Val Arg Ala Cys Leu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe						
		500		505		510
Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe						
		515		520		525
Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp						
		530		535		540
Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val						
		545		550		555
Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala						
		565		570		575
Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg						
		580		585		590
Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe						
		595		600		605
Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg						
		610		615		620
Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val						
		625		630		635
Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg						
		645		650		655
Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr						
		660		665		670
Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Val Ala Val Leu						
		675		680		685
Trp Phe Thr Phe Leu Phe Asn Gln Lys Pro Ser Val Ser Phe Arg Gly						

690

695

700

<210> 59
 <211> 2645
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Truncated Protein 2 (ver.2); with Intron Y and
 Alpha

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 cgcgggggacc cggcggtttt ccgcgcgctg gtggcccagt gcctgggtgtg cgtgccctgg 180
 gacgcacggc cccccccgc cccccctcc ttccgccagg tgggcctccc cggggtcggc 240
 gtccggctgg ggttgagggc ggccgggggg aaccagcgac atgcggagag cagcgcaggc 300
 gactcagggc gcttcccccg caggtgtcct gcctgaagga gctgggtggc cgagtgtgc 360
 agaggctgtg cgagcgcggc gcgaagaacg tgctggcctt cggcttcgcg ctgctggacg 420
 gggcccgcg gggccccccc gaggccttca ccaccagcgt gcgcagctac ctgcccaaca 480
 cggtgaccga cgcactgcgg gggagcgggg cgtgggggct gctgctgcgc cgcgtgggcg 540
 acgacgtgct ggttcacctg ctggcacgct gcgcgctctt tgtgctggtg gctcccagct 600
 gcgcctacca ggtgtgcggg ccgcgcgtgt accagctcgg cgtgccact caggcccggc 660
 ccccgccaca cgctagtga cccgaaggc gtctgggatg cgaacgggccc tggaaaccata 720
 gcgtcaggga ggccggggtc cccctgggccc tgccagcccc ggggtgcgag aggcgcgggg 780
 gcagtgccag ccgaagtctg ccgttgccca agagggccag gcgtggcgct gcccctgagc 840
 cggagcggac gcccgttggg caggggtcct gggcccaccc gggcaggacg cgtggaccga 900
 gtgaccgtgg tttctgtgtg gtgtcacctg ccagaccgcg cgaagaagcc acctctttgg 960
 aggggtgcgt ctctggcacg cgcactccc acccatccgt gggccgccag caccacgcgg 1020
 gcccccatc cacatcgcg ccaccacgtc cctgggacac gccttgtccc ccggtgtacg 1080
 ccgagaccaa gcaattcctc tactcctcag gcgacaagga gcagctgcgg cctccttcc 1140
 tactcagctc tctgaggccc agcctgactg gcgctcggag gctcgtggag accatctttc 1200
 tgggttccag gccctggatg ccagggactc cccgcagggt gccccgcctg cccagcgt 1260
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 gtgcccggga gaagccccag ggctctgtgg cggccccga ggaggaggac acagaccccc 1440
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 gggcctgct gcgcgggctg gtgccccag gcctctgggg ctccaggcac aacgaacgcc 1560
 gcttctcag gaacaccaag aagttcatct cctggggaa gcatgccaag ctctcgtgc 1620
 aggagctgac gtggaagatg agcgtgcggg actgcgctt gctgcgcagg agcccagggg 1680
 ttggctgtgt tccggccgca gagcaccgtc tgcgtgagga gatcctggcc aagttcctgc 1740
 actggctgat gagtgtgtac gtcgtcagac tgctcaggtc tttcttttat gtcacggaga 1800
 ccacgtttca aaagaacagg ctctttttct accggaagag tgtctggagc aagttgcaaa 1860
 gcattggaat cagacagcac ttgaagaggc tgcaagtgcg ggagctgtcg gaagcagagg 1920
 tcaggcagca tcgggaagcc agggccgccc tgctgacgtc cagactccgc ttcacccca 1980
 agcctgacgg cgtcgccggc attgtgaaca tggactacgt cgtgggagcc agaacgttcc 2040
 gcagagaaaa gagggccgag cgtctcacct cgagggtgaa ggcactgttc agcgtgtca 2100
 actacgagcg ggcgcggcgc cccggcctcc tgggcgcctc tgtgctgggc ctggacgata 2160
 tccacagggc ctggcgcacc ttcgtgtgc gtgtgcgggc ccaggacccg ccgcctgagc 2220
 tgtactttgt caaggtggat gtgacgggcg cgtacgacac catccccag gacaggctca 2280
 cggaggtcat cgcagcacc atcaaacccc agaacacgta ctgcgtgcgt cggatgccg 2340
 tgggtccagaa ggccgcccac gggcacgtcc gcaaggcctt caagagccac gtcctacgtc 2400
 cagtgccagg ggatcccga gggctccatc ctctccacgc tgctctgcag cctgtgtac 2460

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ggcgacatgg agaacaagct gtttgcgggg attcggcggg acgggctgct cctgcgtttg 2520
gtggatgatt tcttgttggg gacacctcac ctcacccacg cgaaaacctt cctcaggacc 2580
ctggtccgag gtgtccctga gtatggctgc gtggagaact tgcggaagac agtggagaac 2640
ttccc                                           2645

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<210> 60

<211> 841

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein 2 (ver.2); encoded by SEQ ID
NO:59, with Intron Y ORF1

<400> 60

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Met  Pro  Arg  Ala  Pro  Arg  Cys  Arg  Ala  Val  Arg  Ser  Leu  Leu  Arg  Ser
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His  Thr  Arg  Glu  Val  Leu  Pro  Leu  Ala  Thr  Phe  Val  Arg  Arg  Leu  Gly
          20              25              30

Pro  Gln  Gly  Trp  Arg  Leu  Val  Gln  Arg  Gly  Asp  Pro  Ala  Ala  Phe  Arg
          35              40              45

Ala  Leu  Val  Ala  Gln  Cys  Leu  Val  Cys  Val  Pro  Trp  Asp  Ala  Arg  Pro
  50              55              60

Pro  Pro  Ala  Ala  Pro  Ser  Phe  Arg  Gln  Val  Gly  Leu  Pro  Gly  Val  Gly
  65              70              75              80

Val  Arg  Leu  Gly  Leu  Arg  Ala  Ala  Gly  Gly  Asn  Gln  Arg  His  Ala  Glu
          85              90              95

Ser  Ser  Ala  Gly  Asp  Ser  Gly  Arg  Phe  Pro  Arg  Arg  Ser  Cys  Leu  Lys
          100             105             110

Glu  Leu  Val  Ala  Arg  Val  Leu  Gln  Arg  Leu  Cys  Glu  Arg  Gly  Ala  Lys
          115             120             125

Asn  Val  Leu  Ala  Phe  Gly  Phe  Ala  Leu  Leu  Asp  Gly  Ala  Arg  Gly  Gly
          130             135             140

Pro  Pro  Glu  Ala  Phe  Thr  Thr  Ser  Val  Arg  Ser  Tyr  Leu  Pro  Asn  Thr
          145             150             155             160

Val  Thr  Asp  Ala  Leu  Arg  Gly  Ser  Gly  Ala  Trp  Gly  Leu  Leu  Leu  Arg
          165             170             175

Arg  Val  Gly  Asp  Asp  Val  Leu  Val  His  Leu  Leu  Ala  Arg  Cys  Ala  Leu
          180             185             190

Phe  Val  Leu  Val  Ala  Pro  Ser  Cys  Ala  Tyr  Gln  Val  Cys  Gly  Pro  Pro
          195             200             205

Leu  Tyr  Gln  Leu  Gly  Ala  Ala  Thr  Gln  Ala  Arg  Pro  Pro  Pro  His  Ala
          210             215             220

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Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
 225 230 235 240
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
 245 250 255
 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
 260 265 270
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 275 280 285
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
 290 295 300
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 305 310 315 320
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 325 330 335
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
 340 345 350
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
 355 360 365
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
 370 375 380
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
 385 390 395 400
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
 405 410 415
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
 420 425 430
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
 435 440 445
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
 450 455 460
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
 465 470 475 480
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
 675 680 685
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
 690 695 700
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
 705 710 715 720
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
 725 730 735
 Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp
 740 745 750
 Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys
 755 760 765
 Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala
 770 775 780
 Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Leu Arg Pro
 785 790 795 800
 Val Pro Gly Asp Pro Ala Gly Leu His Pro Leu His Ala Ala Leu Gln
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 Pro Val Leu Arg Arg His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala
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Gly Arg Ala Ala Pro Ala Phe Val Gly
835 840

<210> 61
<211> 756
<212> PRT
<213> Homo sapiens

<220>
<223> Truncated Protein 2 (ver.2); encoded by SEQ ID
NO:59 with Intron Y ORF2 after the termination
codon

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Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
35 40 45
Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
50 55 60
Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
65 70 75 80
Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
85 90 95
Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
100 105 110
Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
115 120 125
Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg
130 135 140
Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
145 150 155 160
Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser
165 170 175
Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala
180 185 190
Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
195 200 205
Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro
210 215 220

Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu	Gly	Ala	Leu	Ser	Gly	225	230	235	240
Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln	His	His	Ala	Gly	Pro	245	250	255	
Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp	Thr	Pro	Cys	Pro	Pro	260	265	270	
Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser	Ser	Gly	Asp	Lys	Glu	275	280	285	
Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu	Arg	Pro	Ser	Leu	Thr	290	295	300	
Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu	Gly	Ser	Arg	Pro	Trp	305	310	315	320
Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu	Pro	Gln	Arg	Tyr	Trp	325	330	335	
Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Gly	Asn	His	Ala	Gln	Cys		340	345	350	
Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro	Leu	Arg	Ala	Ala	Val	355	360	365	
Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys	Pro	Gln	Gly	Ser	Val	370	375	380	
Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg	Arg	Leu	Val	Gln	Leu	385	390	395	400
Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	Tyr	Gly	Phe	Val	Arg	Ala	405	410	415	
Cys	Leu	Arg	Arg	Leu	Val	Pro	Pro	Gly	Leu	Trp	Gly	Ser	Arg	His	Asn	420	425	430	
Glu	Arg	Arg	Phe	Leu	Arg	Asn	Thr	Lys	Lys	Phe	Ile	Ser	Leu	Gly	Lys	435	440	445	
His	Ala	Lys	Leu	Ser	Leu	Gln	Glu	Leu	Thr	Trp	Lys	Met	Ser	Val	Arg	450	455	460	
Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val	Gly	Cys	Val	Pro	Ala	465	470	475	480
Ala	Glu	His	Arg	Leu	Arg	Glu	Glu	Ile	Leu	Ala	Lys	Phe	Leu	His	Trp	485	490	495	
Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg	Ser	Phe	Phe	Tyr	Val	500	505	510	
Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe	Phe	Tyr	Arg	Lys	Ser	515	520	525	

Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg
 530 535 540
 Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu
 545 550 555 560
 Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
 565 570 575
 Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg
 580 585 590
 Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys
 595 600 605
 Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu
 610 615 620
 Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg
 625 630 635 640
 Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr
 645 650 655
 Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp
 660 665 670
 Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr
 675 680 685
 Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val
 690 695 700
 Arg Lys Ala Phe Lys Ser His Val Leu Arg Pro Val Pro Gly Asp Pro
 705 710 715 720
 Ala Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val Leu Arg Arg
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 His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala Gly Arg Ala Ala Pro
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 Ala Phe Val Gly
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<210> 62
 <211> 841
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Truncated Protein 2 (ver.2); encoded by SEQ ID NO:
 59 with Intron Y ORF3

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Pro Gln Gly	Trp Arg Leu Val	Gln Arg Gly Asp Pro	Ala Ala Phe Arg
	35	40	45
Ala Leu Val	Ala Gln Cys Leu	Val Cys Val Pro Trp	Asp Ala Arg Pro
	50	55	60
Pro Pro Ala	Ala Pro Ser Phe	Arg Gln Val Pro Pro	Arg Gly Arg Arg
	65	70	75
Pro Ala Gly	Val Glu Gly Gly	Arg Gly Glu Pro Ala	Thr Cys Gly Glu
	85	90	95
Gln Arg Arg	Arg Leu Arg Ala	Leu Pro Pro Gln	Val Ser Cys Leu Lys
	100	105	110
Glu Leu Val	Ala Arg Val Leu	Gln Arg Leu Cys	Glu Arg Gly Ala Lys
	115	120	125
Asn Val Leu	Ala Phe Gly Phe	Ala Leu Leu Asp	Gly Ala Arg Gly Gly
	130	135	140
Pro Pro Glu	Ala Phe Thr Thr	Ser Val Arg Ser Tyr	Leu Pro Asn Thr
	145	150	155
Val Thr Asp	Ala Leu Arg Gly	Ser Gly Ala Trp	Gly Leu Leu Leu Arg
	165	170	175
Arg Val Gly	Asp Asp Val Leu	Val His Leu Leu	Ala Arg Cys Ala Leu
	180	185	190
Phe Val Leu	Val Ala Pro Ser	Cys Ala Tyr Gln	Val Cys Gly Pro Pro
	195	200	205
Leu Tyr Gln	Leu Gly Ala Ala	Thr Gln Ala Arg	Pro Pro Pro His Ala
	210	215	220
Ser Gly Pro	Arg Arg Arg Leu	Gly Cys Glu Arg	Ala Trp Asn His Ser
	225	230	235
Val Arg Glu	Ala Gly Val Pro	Leu Gly Leu Pro	Ala Pro Gly Ala Arg
	245	250	255
Arg Arg Gly	Gly Ser Ala Ser	Arg Ser Leu Pro	Leu Pro Lys Arg Pro
	260	265	270
Arg Arg Gly	Ala Ala Pro Glu	Pro Glu Arg Thr	Pro Val Gly Gln Gly
	275	280	285
Ser Trp Ala	His Pro Gly Arg	Thr Arg Gly Pro	Ser Asp Arg Gly Phe
	290	295	300
Cys Val Val	Ser Pro Ala Arg	Pro Ala Glu Glu	Ala Thr Ser Leu Glu

305		310		315		320									
Gly	Ala	Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln
				325					330					335	
His	His	Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp
			340					345					350		
Thr	Pro	Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser
		355					360					365			
Ser	Gly	Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu
	370					375					380				
Arg	Pro	Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu
385					390					395					400
Gly	Ser	Arg	Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu
				405					410					415	
Pro	Gln	Arg	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly
			420					425					430		
Asn	His	Ala	Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro
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Leu	Arg	Ala	Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys
	450					455					460				
Pro	Gln	Gly	Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg
465					470					475					480
Arg	Leu	Val	Gln	Leu	Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	Tyr
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Gly	Phe	Val	Arg	Ala	Cys	Leu	Arg	Arg	Leu	Val	Pro	Pro	Gly	Leu	Trp
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Gly	Ser	Arg	His	Asn	Glu	Arg	Arg	Phe	Leu	Arg	Asn	Thr	Lys	Lys	Phe
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Ile	Ser	Leu	Gly	Lys	His	Ala	Lys	Leu	Ser	Leu	Gln	Glu	Leu	Thr	Trp
	530					535					540				
Lys	Met	Ser	Val	Arg	Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val
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Gly	Cys	Val	Pro	Ala	Ala	Glu	His	Arg	Leu	Arg	Glu	Glu	Ile	Leu	Ala
				565					570					575	
Lys	Phe	Leu	His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg
			580					585					590		
Ser	Phe	Phe	Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe
		595					600					605			
Phe	Tyr	Arg	Lys	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile	Arg

610	615	620
Gln His Leu Lys Arg Val	Gln Leu Arg Glu Leu	Ser Glu Ala Glu Val
625	630	635 640
Arg Gln His Arg Glu Ala Arg Pro Ala	Leu Leu Thr Ser Arg Leu Arg	
	645 650	655
Phe Ile Pro Lys Pro Asp Gly Leu Arg	Pro Ile Val Asn Met Asp Tyr	
	660 665	670
Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg	Ala Glu Arg Leu	
	675 680	685
Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu	Asn Tyr Glu Arg Ala	
	690 695	700
Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile		
705	710 715	720
His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro		
	725 730	735
Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp		
	740 745	750
Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys		
	755 760	765
Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala		
	770 775	780
Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Leu Arg Pro		
785	790 795	800
Val Pro Gly Asp Pro Ala Gly Leu His Pro Leu His Ala Ala Leu Gln		
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Pro Val Leu Arg Arg His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala		
	820 825	830
Gly Arg Ala Ala Pro Ala Phe Val Gly		
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<210> 63
 <211> 3500
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Reference Protein (ver.2); with Introns Y, Alpha
 and Beta

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cgcggggacc	cggcggcttt	ccgcgcgctg	gtggcccagt	gcctggtgtg	cgtgccctgg	180
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<210> 64
 <211> 1165
 <212> PRT
 <213> Homo sapiens

<220>

<223> Reference Protein (ver.2); encoded by SEQ ID NO:63
 with Intron Y ORF1

<400> 64

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Pro  Pro  Ala  Ala  Pro  Ser  Phe  Arg  Gln  Val  Gly  Leu  Pro  Gly  Val  Gly
 65              70              75              80

Val  Arg  Leu  Gly  Leu  Arg  Ala  Ala  Gly  Gly  Asn  Gln  Arg  His  Ala  Glu
                85              90              95

Ser  Ser  Ala  Gly  Asp  Ser  Gly  Arg  Phe  Pro  Arg  Arg  Ser  Cys  Leu  Lys
                100              105              110

Glu  Leu  Val  Ala  Arg  Val  Leu  Gln  Arg  Leu  Cys  Glu  Arg  Gly  Ala  Lys
 115              120              125

Asn  Val  Leu  Ala  Phe  Gly  Phe  Ala  Leu  Leu  Asp  Gly  Ala  Arg  Gly  Gly
 130              135              140

Pro  Pro  Glu  Ala  Phe  Thr  Thr  Ser  Val  Arg  Ser  Tyr  Leu  Pro  Asn  Thr
 145              150              155              160

Val  Thr  Asp  Ala  Leu  Arg  Gly  Ser  Gly  Ala  Trp  Gly  Leu  Leu  Leu  Arg
                165              170              175

Arg  Val  Gly  Asp  Asp  Val  Leu  Val  His  Leu  Leu  Ala  Arg  Cys  Ala  Leu
                180              185              190

Phe  Val  Leu  Val  Ala  Pro  Ser  Cys  Ala  Tyr  Gln  Val  Cys  Gly  Pro  Pro
 195              200              205

Leu  Tyr  Gln  Leu  Gly  Ala  Ala  Thr  Gln  Ala  Arg  Pro  Pro  Pro  His  Ala
 210              215              220

Ser  Gly  Pro  Arg  Arg  Arg  Leu  Gly  Cys  Glu  Arg  Ala  Trp  Asn  His  Ser
 225              230              235              240

Val  Arg  Glu  Ala  Gly  Val  Pro  Leu  Gly  Leu  Pro  Ala  Pro  Gly  Ala  Arg

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245										250					255				
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Arg	Arg	Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly				
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Ser	Trp	Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe				
	290					295					300								
Cys	Val	Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu				
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His	His	Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp				
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Thr	Pro	Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser				
		355					360					365							
Ser	Gly	Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu				
	370					375					380								
Arg	Pro	Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu				
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Pro	Gln	Arg	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly				
			420					425					430						
Asn	His	Ala	Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro				
		435					440					445							
Leu	Arg	Ala	Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys				
	450					455					460								
Pro	Gln	Gly	Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg				
465					470					475					480				
Arg	Leu	Val	Gln	Leu	Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	Tyr				
				485					490					495					
Gly	Phe	Val	Arg	Ala	Cys	Leu	Arg	Arg	Leu	Val	Pro	Pro	Gly	Leu	Trp				
			500					505					510						
Gly	Ser	Arg	His	Asn	Glu	Arg	Arg	Phe	Leu	Arg	Asn	Thr	Lys	Lys	Phe				
		515					520					525							
Ile	Ser	Leu	Gly	Lys	His	Ala	Lys	Leu	Ser	Leu	Gln	Glu	Leu	Thr	Trp				
	530					535					540								
Lys	Met	Ser	Val	Arg	Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val				

545		550		555		560
Gly Cys Val Pro	Ala 565	Ala Glu His Arg	Leu 570	Arg Glu Glu Ile	Leu 575	Ala
Lys Phe Leu	His 580	Trp Leu Met Ser	Val 585	Tyr Val Val Glu	Leu 590	Leu Arg
Ser Phe Phe	Tyr 595	Val Thr Glu Thr	Thr 600	Phe Gln Lys Asn	Arg 605	Leu Phe
Phe Tyr Arg	Lys 610	Ser Val Trp Ser	Lys 615	Leu Gln Ser Ile	Gly 620	Ile Arg
Gln His Leu	Lys 625	Arg Val Gln Leu	Arg 630	Glu Leu Ser Glu	Ala 635	Glu Val
Arg Gln His	Arg 645	Glu Ala Arg Pro	Ala 650	Leu Leu Thr Ser	Arg 655	Leu Arg
Phe Ile Pro	Lys 660	Pro Asp Gly Leu	Arg 665	Pro Ile Val Asn	Met 670	Asp Tyr
Val Val Gly	Ala 675	Arg Thr Phe Arg	Arg 680	Glu Lys Arg Ala	Glu 685	Arg Leu
Thr Ser Arg	Val 690	Lys Ala Leu Phe	Ser 695	Val Leu Asn Tyr	Glu 700	Arg Ala
Arg Arg Pro	Gly 705	Leu Leu Gly Ala	Ser 710	Val Leu Gly Leu	Asp 715	Asp Ile
His Arg Ala	Trp 725	Arg Thr Phe Val	Leu 730	Arg Val Arg Ala	Gln 735	Asp Pro
Pro Pro Glu	Leu 740	Tyr Phe Val Lys	Val 745	Asp Val Thr Gly	Ala 750	Tyr Asp
Thr Ile Pro	Gln 755	Asp Arg Leu Thr	Glu 760	Val Ile Ala Ser	Ile 765	Ile Lys
Pro Gln Asn	Thr 770	Tyr Cys Val Arg	Arg 775	Tyr Ala Val Val	Gln 780	Lys Ala
Ala His Gly	His 785	Val Arg Lys Ala	Phe 790	Lys Ser His Val	Ser 795	Thr Leu
Thr Asp Leu	Gln 805	Pro Tyr Met Arg	Gln 810	Phe Val Ala His	Leu 815	Gln Glu
Thr Ser Pro	Leu 820	Arg Asp Ala Val	Val 825	Ile Glu Gln Ser	Ser 830	Ser Leu
Asn Glu Ala	Ser 835	Ser Gly Leu Phe	Asp 840	Val Phe Leu Arg	Phe 845	Met Cys
His His Ala	Val 850	Arg Ile Arg Gly	Lys 855	Ser Tyr Val Gln	Cys 860	Gln Gly

850		855		860
Ile Pro Gln Gly Ser	Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr			
865	870	875	880	
Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu				
	885	890	895	
Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr				
	900	905	910	
His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr				
	915	920	925	
Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu				
	930	935	940	
Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly				
	945	950	955	960
Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val				
	965	970	975	
Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu				
	980	985	990	
Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu				
	995	1000	1005	
Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln				
	1010	1015	1020	
Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu				
	1025	1030	1035	1040
Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His				
	1045	1050	1055	
Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp				
	1060	1065	1070	
Thr Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser				
	1075	1080	1085	
Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln				
	1090	1095	1100	
Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val				
	1105	1110	1115	1120
Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu				
	1125	1130	1135	
Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala				
	1140	1145	1150	
Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp				

1155

1160

1165

<210> 65
 <211> 1081
 <212> PRT
 <213> Homo sapiens

<220>

<223> Reference Protein (ver.2); encoded by SEQ ID NO:63
 with Intron Y ORF2 after the termination codon

<400> 65

Gly	Arg	Pro	Gly	Gly	Thr	Ser	Asp	Met	Arg	Arg	Ala	Ala	Gln	Ala	Thr
1				5					10					15	
Gln	Gly	Ala	Ser	Pro	Ala	Gly	Ser	Cys	Leu	Lys	Glu	Leu	Val	Ala	Arg
			20					25					30		
Val	Leu	Gln	Arg	Leu	Cys	Glu	Arg	Gly	Ala	Lys	Asn	Val	Leu	Ala	Phe
	35						40					45			
Gly	Phe	Ala	Leu	Leu	Asp	Gly	Ala	Arg	Gly	Gly	Pro	Pro	Glu	Ala	Phe
	50					55					60				
Thr	Thr	Ser	Val	Arg	Ser	Tyr	Leu	Pro	Asn	Thr	Val	Thr	Asp	Ala	Leu
	65					70				75					80
Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu	Leu	Arg	Arg	Val	Gly	Asp	Asp
				85					90					95	
Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu	Phe	Val	Leu	Val	Ala
			100					105					110		
Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro	Leu	Tyr	Gln	Leu	Gly
		115					120					125			
Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala	Ser	Gly	Pro	Arg	Arg
		130				135					140				
Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser	Val	Arg	Glu	Ala	Gly
145					150					155					160
Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg	Arg	Arg	Gly	Gly	Ser
				165					170					175	
Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro	Arg	Arg	Gly	Ala	Ala
			180					185					190		
Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly	Ser	Trp	Ala	His	Pro
	195						200					205			
Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe	Cys	Val	Val	Ser	Pro
	210					215					220				
Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu	Gly	Ala	Leu	Ser	Gly
225					230					235					240

Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro
 245 250 255
 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro
 260 265 270
 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu
 275 280 285
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr
 290 295 300
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp
 305 310 315 320
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp
 325 330 335
 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys
 340 345 350
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val
 355 360 365
 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val
 370 375 380
 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu
 385 390 395 400
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala
 405 410 415
 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
 420 425 430
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
 435 440 445
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
 450 455 460
 Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
 465 470 475 480
 Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
 485 490 495
 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
 500 505 510
 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
 515 520 525
 Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg
 530 535 540

Val	Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu	Val	Arg	Gln	His	Arg	Glu	545	550	555	560
Ala	Arg	Pro	Ala	Leu	Leu	Thr	Ser	Arg	Leu	Arg	Phe	Ile	Pro	Lys	Pro	565	570	575	
Asp	Gly	Leu	Arg	Pro	Ile	Val	Asn	Met	Asp	Tyr	Val	Val	Gly	Ala	Arg	580	585	590	
Thr	Phe	Arg	Arg	Glu	Lys	Arg	Ala	Glu	Arg	Leu	Thr	Ser	Arg	Val	Lys	595	600	605	
Ala	Leu	Phe	Ser	Val	Leu	Asn	Tyr	Glu	Arg	Ala	Arg	Arg	Pro	Gly	Leu	610	615	620	
Leu	Gly	Ala	Ser	Val	Leu	Gly	Leu	Asp	Asp	Ile	His	Arg	Ala	Trp	Arg	625	630	635	640
Thr	Phe	Val	Leu	Arg	Val	Arg	Ala	Gln	Asp	Pro	Pro	Pro	Glu	Leu	Tyr	645	650	655	
Phe	Val	Lys	Val	Asp	Val	Thr	Gly	Ala	Tyr	Asp	Thr	Ile	Pro	Gln	Asp	660	665	670	
Arg	Leu	Thr	Glu	Val	Ile	Ala	Ser	Ile	Ile	Lys	Pro	Gln	Asn	Thr	Tyr	675	680	685	
Cys	Val	Arg	Arg	Tyr	Ala	Val	Val	Gln	Lys	Ala	Ala	His	Gly	His	Val	690	695	700	
Arg	Lys	Ala	Phe	Lys	Ser	His	Val	Ser	Thr	Leu	Thr	Asp	Leu	Gln	Pro	705	710	715	720
Tyr	Met	Arg	Gln	Phe	Val	Ala	His	Leu	Gln	Glu	Thr	Ser	Pro	Leu	Arg	725	730	735	
Asp	Ala	Val	Val	Ile	Glu	Gln	Ser	Ser	Ser	Leu	Asn	Glu	Ala	Ser	Ser	740	745	750	
Gly	Leu	Phe	Asp	Val	Phe	Leu	Arg	Phe	Met	Cys	His	His	Ala	Val	Arg	755	760	765	
Ile	Arg	Gly	Lys	Ser	Tyr	Val	Gln	Cys	Gln	Gly	Ile	Pro	Gln	Gly	Ser	770	775	780	
Ile	Leu	Ser	Thr	Leu	Leu	Cys	Ser	Leu	Cys	Tyr	Gly	Asp	Met	Glu	Asn	785	790	795	800
Lys	Leu	Phe	Ala	Gly	Ile	Arg	Arg	Asp	Gly	Leu	Leu	Leu	Arg	Leu	Val	805	810	815	
Asp	Asp	Phe	Leu	Leu	Val	Thr	Pro	His	Leu	Thr	His	Ala	Lys	Thr	Phe	820	825	830	
Leu	Arg	Thr	Leu	Val	Arg	Gly	Val	Pro	Glu	Tyr	Gly	Cys	Val	Val	Asn	835	840	845	

Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly
 850 855 860
 Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys
 865 870 875 880
 Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser
 885 890 895
 Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn Arg Gly
 900 905 910
 Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu Arg
 915 920 925
 Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu Gln
 930 935 940
 Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala Tyr Arg
 945 950 955 960
 Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val Trp Lys
 965 970 975
 Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu Cys
 980 985 990
 Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly Ala Lys
 995 1000 1005
 Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu Cys His
 1010 1015 1020
 Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr Val Pro
 1025 1030 1035 1040
 Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg Lys Leu
 1045 1050 1055
 Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro Ala Leu
 1060 1065 1070
 Pro Ser Asp Phe Lys Thr Ile Leu Asp
 1075 1080

<210> 66
 <211> 1165
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Reference Protein (ver.2); encoded by SEQ ID NO:63
 with Intron Y ORF3

<400> 66

Met	Pro	Arg	Ala	Pro	Arg	Cys	Arg	Ala	Val	Arg	Ser	Leu	Leu	Arg	Ser	1	5	10	15
His	Tyr	Arg	Glu	Val	Leu	Pro	Leu	Ala	Thr	Phe	Val	Arg	Arg	Leu	Gly	20	25	30	
Pro	Gln	Gly	Trp	Arg	Leu	Val	Gln	Arg	Gly	Asp	Pro	Ala	Ala	Phe	Arg	35	40	45	
Ala	Leu	Val	Ala	Gln	Cys	Leu	Val	Cys	Val	Pro	Trp	Asp	Ala	Arg	Pro	50	55	60	
Pro	Pro	Ala	Ala	Pro	Ser	Phe	Arg	Gln	Val	Pro	Pro	Arg	Gly	Arg	Arg	65	70	75	80
Pro	Ala	Gly	Val	Glu	Gly	Gly	Arg	Gly	Glu	Pro	Ala	Thr	Cys	Gly	Glu	85	90	95	
Gln	Arg	Arg	Arg	Leu	Arg	Ala	Leu	Pro	Pro	Gln	Val	Ser	Cys	Leu	Lys	100	105	110	
Glu	Leu	Val	Ala	Arg	Val	Leu	Gln	Arg	Leu	Cys	Glu	Arg	Gly	Ala	Lys	115	120	125	
Asn	Val	Leu	Ala	Phe	Gly	Phe	Ala	Leu	Leu	Asp	Gly	Ala	Arg	Gly	Gly	130	135	140	
Pro	Pro	Glu	Ala	Phe	Thr	Thr	Ser	Val	Arg	Ser	Tyr	Leu	Pro	Asn	Thr	145	150	155	160
Val	Thr	Asp	Ala	Leu	Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu	Leu	Arg	165	170	175	
Arg	Val	Gly	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu	180	185	190	
Phe	Val	Leu	Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro	195	200	205	
Leu	Tyr	Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala	210	215	220	
Ser	Gly	Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser	225	230	235	240
Val	Arg	Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg	245	250	255	
Arg	Arg	Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro	260	265	270	
Arg	Arg	Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly	275	280	285	
Ser	Trp	Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe	290	295	300	

Cys	Val	Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu	305	310	315	320
Gly	Ala	Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln	325	330	335	
His	His	Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp	340	345	350	
Thr	Pro	Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser	355	360	365	
Ser	Gly	Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu	370	375	380	
Arg	Pro	Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu	385	390	395	400
Gly	Ser	Arg	Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu	405	410	415	
Pro	Gln	Arg	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly	420	425	430	
Asn	His	Ala	Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro	435	440	445	
Leu	Arg	Ala	Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys	450	455	460	
Pro	Gln	Gly	Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg	465	470	475	480
Arg	Leu	Val	Gln	Leu	Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	Tyr	485	490	495	
Gly	Phe	Val	Arg	Ala	Cys	Leu	Arg	Arg	Leu	Val	Pro	Pro	Gly	Leu	Trp	500	505	510	
Gly	Ser	Arg	His	Asn	Glu	Arg	Arg	Phe	Leu	Arg	Asn	Thr	Lys	Lys	Phe	515	520	525	
Ile	Ser	Leu	Gly	Lys	His	Ala	Lys	Leu	Ser	Leu	Gln	Glu	Leu	Thr	Trp	530	535	540	
Lys	Met	Ser	Val	Arg	Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val	545	550	555	560
Gly	Cys	Val	Pro	Ala	Ala	Glu	His	Arg	Leu	Arg	Glu	Glu	Ile	Leu	Ala	565	570	575	
Lys	Phe	Leu	His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg	580	585	590	
Ser	Phe	Phe	Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe	595	600	605	

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
 675 680 685
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
 690 695 700
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
 705 710 715 720
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
 725 730 735
 Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp
 740 745 750
 Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys
 755 760 765
 Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala
 770 775 780
 Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu
 785 790 795 800
 Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu
 805 810 815
 Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu
 820 825 830
 Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys
 835 840 845
 His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly
 850 855 860
 Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr
 865 870 875 880
 Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu
 885 890 895
 Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr
 900 905 910

His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr
 915 920 925
 Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu
 930 935 940
 Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly
 945 950 955 960
 Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val
 965 970 975
 Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu
 980 985 990
 Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu
 995 1000 1005
 Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln
 1010 1015 1020
 Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu
 1025 1030 1035 1040
 Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His
 1045 1050 1055
 Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp
 1060 1065 1070
 Thr Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser
 1075 1080 1085
 Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln
 1090 1095 1100
 Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val
 1105 1110 1115 1120
 Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu
 1125 1130 1135
 Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala
 1140 1145 1150
 Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 1155 1160 1165

<210> 67
 <211> 3173
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Truncated Protein (ver.2); with Introns Y, Alpha,
 Beta and 2

<400> 67

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gtgctgccgc	tggccacgtt	cgtgcggcgc	ctggggcccc	agggctggcg	gctggtgcag	120
cgcggggacc	cggcggcttt	ccgcgcgctg	gtggcccagt	gcctggtgtg	cgtgccctgg	180
gacgcacggc	cgccccccgc	cgccccctcc	ttccgccagg	tgggcctccc	cggggtcggc	240
gtccggctgg	ggttgagggc	ggccgggggg	aaccagcgac	atgcggagag	cagcgcaggc	300
gactcagggc	gcttcccccg	caggtgtcct	gcctgaagga	gctggtggcc	cgagtgtgc	360
agaggctgtg	cgagcgcggc	gcgaagaacg	tgtggcctt	cggcttcgcg	ctgctggacg	420
gggcccgcgg	gggccccccc	gaggccttca	ccaccagcgt	gcgcagctac	ctgcccacaa	480
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acgacgtgct	ggttcacctg	ctggcacgct	gcgcgctctt	tgtgctggtg	gctcccagct	600
gcgcctacca	ggtgtgcggg	ccgcgcgctg	accagctcgg	cgctgccact	caggccccgc	660
ccccgccaca	cgctagtggg	ccccgaaggc	gtctgggatg	cgaacggggc	tggaaccata	720
gcgtcagggg	ggccgggggtc	ccccggggcc	tgccagcccc	gggtgcgagg	aggcgcgggg	780
gcagtgccag	ccgaagtctg	ccgttgccca	agaggcccg	gcgtggcgct	gccccgtgac	840
cggagcggac	gcccgttggg	caggggtcct	gggcccaccc	gggcaggacg	cgtggaccga	900
gtgacgcgtg	tttctgtgtg	gtgtcacctg	ccagaccgcg	cgaagaagcc	acctcttttg	960
aggggtgcgct	ctctggcacg	cgccactccc	acccatccgt	gggcccgcag	caccacgcgg	1020
gccccccatc	cacatcgcg	ccaccacgtc	cctgggacac	gccttgtccc	ccggtgtacg	1080
ccgagaccaa	gcacttcctc	tactcctcag	gcgacaagga	gcagctgcgg	ccctccttcc	1140
tactcagctc	tctgaggccc	agcctgactg	gcgctcggag	gctcgtggag	accatctttc	1200
tgggttccag	gccctggatg	ccagggactc	cccgacaggt	gccccgcctg	ccccagcgtc	1260
actggcaaat	gcggccccctg	tttctggagc	tgtctgggaa	ccacgcgcag	tgccccacg	1320
gggtgctcct	caagacgcac	tgcccgcgtc	gagctgcggt	caccccgaca	gccggtgtct	1380
gtgcccggga	gaagccccag	ggctctgtgg	cgccccccga	ggaggaggac	acagaccccc	1440
gtgccttgt	gcagctgctc	cgccagcaca	gcagcccctg	gcagggtgtac	ggcttcgtgc	1500
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gcttcctcag	gaacaccaag	aagttcatct	ccctggggaa	gcatgccaa	ctctcgctgc	1620
aggagctgac	gtggaagatg	agcgtgcggg	actgcgcttg	gctgcgcagg	agcccagggg	1680
ttggctgtgt	tccggccgca	gagcaccgtc	tgctgagga	gacccctggc	aagttcctgc	1740
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ccacgtttca	aaagaacagg	ctctttttct	accggaagag	tgtctggagc	aagttgcaaa	1860
gcatttgaat	cagacagcac	ttgaagaggg	tgacgtgcg	ggagctgtcg	gaagcagagg	1920
tcaggcagca	tcgggaagcc	aggccccccc	tgctgacgtc	cagactccgc	ttcatcccca	1980
agcctgacgg	gctgcggccg	attgtgaaca	tggactacgt	cgtgggagcc	agaacgttcc	2040
gcagagaaaa	gagggccgag	cgtctcacct	cgagggtgaa	ggcactgttc	agcgtgtca	2100
actacgagcg	ggcgcgcgcg	cccggcctcc	tgggcgcctc	tgtgctgggc	ctggacgata	2160
tccacagggc	ctggcgcacc	ttcgtgctgc	gtgtgcgggc	ccaggacccg	ccgcctgagc	2220
tgtactttgt	caaggtggat	gtgacggggc	cgtacgacac	catccccag	gacaggtca	2280
cggaggtcat	cgccagcatc	atcaaacc	agaacacgta	ctgcgtgcgt	cggtatgccg	2340
tggtccagaa	ggccgccc	gggcacgtcc	gcaaggcctt	caagagccac	gtctctacct	2400
tgacagacct	ccagccgtac	atgcgacagt	tcgtggctca	cctgcaggag	accagcccg	2460
tgagggatgc	cgctcgtcatc	gagcagagct	cctccctgaa	tgaggccagc	agtggcctct	2520
togacgtctt	cctacgcttc	atgtgccacc	acgccgtgcg	catcaggggc	aagtcctacg	2580
tccagtgcc	ggggatccc	cagggctcca	tcctctccac	gctgctctgc	agcctgtgct	2640
acggcgacat	ggagaacaag	ctgtttgcgg	ggattcggcg	ggacgggctg	ctcctgcgtt	2700
tgggtgatga	tttcttgttg	gtgacacctc	acctcaccca	cgcgaaaacc	ttcctcagga	2760
ccttggtccg	aggtgtccct	gagtatggct	gcgtgggtgaa	cttgccggaag	acagtggtga	2820
acttcctgt	agaagacgag	gcccgtgggtg	gcacggcttt	tgttcagatg	ccggcccacg	2880
gcctattccc	ctgggtgcggc	ctgctgctgg	ataccgggac	cctggagggtg	cagagcgact	2940
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tgcagggccg	ttgcgtccac	ctctgcttcc	gtgtggggca	ggcgactgcc	aatcccaaag	3060
ggtcagatgc	cacaggtg	ccctcgcccc	atctggggct	gagcacaat	gcatctttct	3120
gtgggagtga	gggtgcctca	caacgggagc	agttttctgt	gctatttttg	taa	3173

<210> 68

<211> 982
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Truncated Protein 3 (ver.2); encoded by SEQ ID
 NO:67 with Intron Y ORF1

<400> 68
 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
 1 5 10 15
 His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
 65 70 75 80
 Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
 85 90 95
 Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
 100 105 110
 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
 115 120 125
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
 130 135 140
 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
 145 150 155 160
 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
 165 170 175
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
 180 185 190
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
 195 200 205
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
 210 215 220
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
 225 230 235 240
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
 245 250 255

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
 260 265 270
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 275 280 285
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
 290 295 300
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 305 310 315 320
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 325 330 335
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
 340 345 350
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
 355 360 365
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
 370 375 380
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
 385 390 395 400
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
 405 410 415
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
 420 425 430
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
 435 440 445
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
 450 455 460
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
 465 470 475 480
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
 675 680 685
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
 690 695 700
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
 705 710 715 720
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
 725 730 735
 Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp
 740 745 750
 Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys
 755 760 765
 Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala
 770 775 780
 Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu
 785 790 795 800
 Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu
 805 810 815
 Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu
 820 825 830
 Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys
 835 840 845
 His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly
 850 855 860

Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr
 865 870 875 880
 Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu
 885 890 895
 Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr
 900 905 910
 His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr
 915 920 925
 Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu
 930 935 940
 Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly
 945 950 955 960
 Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val
 965 970 975
 Gln Ser Asp Tyr Ser Arg
 980

<210> 69
 <211> 897
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Truncated Protein 3 (ver.2); encoded by SEQ ID
 NO:67 with Intron Y ORF2 after the termination
 codon

<400> 69
 Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
 1 5 10 15
 Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg
 20 25 30
 Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
 35 40 45
 Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
 50 55 60
 Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
 65 70 75 80
 Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
 85 90 95
 Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
 100 105 110

Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
 420 425 430
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
 435 440 445
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
 450 455 460
 Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
 465 470 475 480
 Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
 485 490 495
 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
 500 505 510
 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
 515 520 525
 Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg
 530 535 540
 Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu
 545 550 555 560
 Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
 565 570 575
 Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg
 580 585 590
 Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys
 595 600 605
 Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu
 610 615 620
 Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg
 625 630 635 640
 Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr
 645 650 655
 Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp
 660 665 670
 Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr
 675 680 685
 Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val
 690 695 700
 Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro
 705 710 715 720

Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg
 725 730 735
 Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser
 740 745 750
 Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala Val Arg
 755 760 765
 Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser
 770 775 780
 Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn
 785 790 795 800
 Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val
 805 810 815
 Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe
 820 825 830
 Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn
 835 840 845
 Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly
 850 855 860
 Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys
 865 870 875 880
 Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser
 885 890 895

Arg

<210> 70
 <211> 982
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Truncated Protein 3 (Ver.2); encoded by SEQ ID
 NO:67 with Intron Y ORF3

<400> 70
 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
 1 5 10 15
 His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro

50					55					60					
Pro 65	Pro	Ala	Ala	Pro	Ser 70	Phe	Arg	Gln	Val	Pro 75	Pro	Arg	Gly	Arg	Arg 80
Pro	Ala	Gly	Val	Glu 85	Gly	Gly	Arg	Gly	Glu 90	Pro	Ala	Thr	Cys	Gly 95	Glu
Gln	Arg	Arg	Arg	Leu 100	Arg	Ala	Leu	Pro 105	Pro	Gln	Val	Ser	Cys	Leu	Lys
Glu	Leu	Val	Ala	Arg	Val	Leu	Gln	Arg	Leu	Cys	Glu	Arg	Gly	Ala	Lys
Asn 130	Val	Leu	Ala	Phe	Gly	Phe 135	Ala	Leu	Leu	Asp	Gly 140	Ala	Arg	Gly	Gly
Pro 145	Pro	Glu	Ala	Phe	Thr 150	Thr	Ser	Val	Arg	Ser 155	Tyr	Leu	Pro	Asn	Thr 160
Val	Thr	Asp	Ala	Leu 165	Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu	Leu	Arg 175
Arg	Val	Gly	Asp 180	Asp	Val	Leu	Val	His 185	Leu	Leu	Ala	Arg	Cys	Ala	Leu
Phe	Val	Leu	Val	Ala	Pro	Ser	Cys 200	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro
Leu 210	Tyr	Gln	Leu	Gly	Ala	Ala 215	Thr	Gln	Ala	Arg	Pro 220	Pro	Pro	His	Ala
Ser 225	Gly	Pro	Arg	Arg	Arg 230	Leu	Gly	Cys	Glu	Arg 235	Ala	Trp	Asn	His	Ser 240
Val	Arg	Glu	Ala	Gly 245	Val	Pro	Leu	Gly	Leu 250	Pro	Ala	Pro	Gly	Ala	Arg 255
Arg	Arg	Gly	Gly 260	Ser	Ala	Ser	Arg	Ser 265	Leu	Pro	Leu	Pro	Lys	Arg	Pro 270
Arg	Arg	Gly 275	Ala	Ala	Pro	Glu	Pro 280	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly
Ser 290	Trp	Ala	His	Pro	Gly	Arg 295	Thr	Arg	Gly	Pro	Ser 300	Asp	Arg	Gly	Phe
Cys 305	Val	Val	Ser	Pro	Ala 310	Arg	Pro	Ala	Glu	Glu 315	Ala	Thr	Ser	Leu	Glu 320
Gly	Ala	Leu	Ser	Gly 325	Thr	Arg	His	Ser	His 330	Pro	Ser	Val	Gly	Arg	Gln 335
His	His	Ala	Gly 340	Pro	Pro	Ser	Thr	Ser 345	Arg	Pro	Pro	Arg	Pro	Trp	Asp 350
Thr	Pro	Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser

355	360	365
Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu		
370	375	380
Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu		
385	390	395
Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu		
405	410	415
Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly		
420	425	430
Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro		
435	440	445
Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys		
450	455	460
Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg		
465	470	475
Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr		
485	490	495
Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp		
500	505	510
Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe		
515	520	525
Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp		
530	535	540
Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val		
545	550	555
Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala		
565	570	575
Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg		
580	585	590
Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe		
595	600	605
Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg		
610	615	620
Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val		
625	630	635
Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg		
645	650	655
Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr		

660					665					670					
Val	Val	Gly	Ala	Arg	Thr	Phe	Arg	Arg	Glu	Lys	Arg	Ala	Glu	Arg	Leu
		675					680					685			
Thr	Ser	Arg	Val	Lys	Ala	Leu	Phe	Ser	Val	Leu	Asn	Tyr	Glu	Arg	Ala
	690					695					700				
Arg	Arg	Pro	Gly	Leu	Leu	Gly	Ala	Ser	Val	Leu	Gly	Leu	Asp	Asp	Ile
705				710						715					720
His	Arg	Ala	Trp	Arg	Thr	Phe	Val	Leu	Arg	Val	Arg	Ala	Gln	Asp	Pro
				725					730					735	
Pro	Pro	Glu	Leu	Tyr	Phe	Val	Lys	Val	Asp	Val	Thr	Gly	Ala	Tyr	Asp
			740					745					750		
Thr	Ile	Pro	Gln	Asp	Arg	Leu	Thr	Glu	Val	Ile	Ala	Ser	Ile	Ile	Lys
		755					760					765			
Pro	Gln	Asn	Thr	Tyr	Cys	Val	Arg	Arg	Tyr	Ala	Val	Val	Gln	Lys	Ala
	770					775					780				
Ala	His	Gly	His	Val	Arg	Lys	Ala	Phe	Lys	Ser	His	Val	Ser	Thr	Leu
785						790					795				800
Thr	Asp	Leu	Gln	Pro	Tyr	Met	Arg	Gln	Phe	Val	Ala	His	Leu	Gln	Glu
				805					810					815	
Thr	Ser	Pro	Leu	Arg	Asp	Ala	Val	Val	Ile	Glu	Gln	Ser	Ser	Ser	Leu
			820				825						830		
Asn	Glu	Ala	Ser	Ser	Gly	Leu	Phe	Asp	Val	Phe	Leu	Arg	Phe	Met	Cys
		835					840					845			
His	His	Ala	Val	Arg	Ile	Arg	Gly	Lys	Ser	Tyr	Val	Gln	Cys	Gln	Gly
	850					855					860				
Ile	Pro	Gln	Gly	Ser	Ile	Leu	Ser	Thr	Leu	Leu	Cys	Ser	Leu	Cys	Tyr
865				870						875					880
Gly	Asp	Met	Glu	Asn	Lys	Leu	Phe	Ala	Gly	Ile	Arg	Arg	Asp	Gly	Leu
				885					890					895	
Leu	Leu	Arg	Leu	Val	Asp	Asp	Phe	Leu	Leu	Val	Thr	Pro	His	Leu	Thr
			900					905					910		
His	Ala	Lys	Thr	Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly	Val	Pro	Glu	Tyr
		915					920					925			
Gly	Cys	Val	Val	Asn	Leu	Arg	Lys	Thr	Val	Val	Asn	Phe	Pro	Val	Glu
	930					935					940				
Asp	Glu	Ala	Leu	Gly	Gly	Thr	Ala	Phe	Val	Gln	Met	Pro	Ala	His	Gly
945				950						955					960
Leu	Phe	Pro	Trp	Cys	Gly	Leu	Leu	Leu	Asp	Thr	Arg	Thr	Leu	Glu	Val

965

970

975

Gln Ser Asp Tyr Ser Arg
980

<210> 71

<211> 3466

<212> DNA

<213> Homo sapiens

<220>

<223> Altered C-Terminus Protein (ver.2); with Introns
Y, Alpha, Beta and 3

<400> 71

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cgcggggacc	cggcggcttt	ccgcgcgctg	gtggcccagt	gcctgggtgtg	cgtgccctgg	180
gacgcacggc	cgccccccgc	cgccccctcc	ttccgccagg	tgggcctccc	cggggtcggc	240
gtccggctgg	ggttgagggc	ggccgggggg	aaccagcgac	atgcggagag	cagcgcaggc	300
gactcagggc	gcttcccccg	caggtgtcct	gcctgaagga	gctgggtggc	cgagtgcctg	360
agaggctgtg	cgagcgcggc	gcgaagaacg	tgetggcctt	cggttcgcg	ctgctggacg	420
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gcgcctacca	ggtgtgcggg	ccgccgctgt	accagctcgg	cgtgccact	caggccccgc	660
ccccgccaca	cgctagtggg	ccccgaaggc	gtctgggatg	cgaacggggc	tggaaaccata	720
gcgtcagggg	ggccgggggtc	cccctggggc	tgccagcccc	gggtgcgagg	aggcgcgggg	780
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cggagcggac	gcccgttggg	caggggtcct	gggcccaccc	gggcaggacg	cgtggaccga	900
gtgaccgtgg	tttctgtgtg	gtgtcacctg	ccagaccgcg	cgaagaagcc	acctctttgg	960
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ccgagacca	gcacttcctc	tactcctcag	gcgacaagga	gcagctgcgg	ccctccttcc	1140
tactcagctc	tctgaggccc	agcctgactg	gcgctcggag	gctcgtggag	accatctttc	1200
tgggttccag	gccctggatg	ccagggactc	cccgcagggt	gccccgcctg	ccccagcgct	1260
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gggtgtcct	caagacgcac	tgcccgtgc	gagctgcggt	caccccagca	gccggtgtct	1380
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gcttcctcag	gaacaccaag	aagttcatct	ccctggggaa	gcatgccaag	ctctcgctgc	1620
aggagctgac	gtggaagatg	agcgtgcggg	actgcgcttg	gctgcgcagg	agcccagggg	1680
ttggctgtgt	tccggccgca	gagcaccgtc	tgcgtgagga	gatcctggcc	aagttcctgc	1740
actggctgat	gagtgtgtac	gtcgtcgagc	tgctcaggtc	tttcttttat	gtcacggaga	1800
ccacgtttca	aaagaacagg	ctctttttct	accggaagag	tgtctggagc	aagttgcaaa	1860
gcattggaat	cagacagcac	ttgaagaggg	tgcagctgcg	ggagctgtcg	gaagcagagg	1920
tcaggcacga	tcggaagccc	aggccccccc	tgtgtacgtc	cagactccgc	ttcatcccca	1980
agcctgacgg	attgtgaaca	tggactacgt	cgtgggagcc	agaacgttcc		2040
gcagagaaaa	gagggccgag	cgtctcacct	cgaggggtgaa	ggcactgttc	agcgtgctca	2100
actacgagcg	ggcgcggcgc	cccggcctcc	tgggcgcctc	tgtgctgggc	ctggacgata	2160
tccacagggc	ctggcgcacc	ttcgtgctgc	gtgtgcgggc	ccaggacccg	ccgcctgagc	2220
tgtactttgt	caaggtggat	gtgacgggcg	cgtacgacac	catccccccag	gacaggctca	2280
cggaggtcat	cgccagcatc	atcaaaccct	agaacacgta	ctgcgtgcgt	cggtatgccg	2340
tggtcagaa	ggccgcccct	gggcacgtcc	gcaaggcctt	caagagccac	gtctctacct	2400
tgacagacct	ccagccgtac	atgcgacagt	tcgtggctca	cctgcaggag	accagcccgc	2460

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tgagggatgc cgtcgtcatc gagcagagct cctccctgaa tgaggccagc agtggcctct 2520
tcgacgtctt cctacgcttc atgtgccacc acgccgtgcg catcaggggc aagtcctacg 2580
tccagtgccg ggggatcccg cagggctcca tcctctccac gctgctctgc agcctgtgct 2640
acggcgacat ggagaacaag ctgtttgcgg ggattcggcg ggacgggctg ctcctgcggt 2700
tggtggatga tttcttggtg gtgacacctc acctcaccca cgcgaaaacc ttcctcagga 2760
ccctggtcgg aggtgtccct gagtatggct gcgtggtgaa cttgcggaag acagtgggtga 2820
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ggaagaaccc cacatttttc ctgctgcgtc tctctgacac ggctccctc tgctactcca 3240
tcctgaaagc caagaacgca gccgaagaaa acatttctgt cgtgactcct gcggtgcttg 3300
ggctggggaca gccagagatg gagccacccc gcagaccgtc ggggtgtgggc agctttcccg 3360
tgtctcctgg gaggggagtt gggctgggcc tgtgactcct cagcctctgt tttcccccag 3420
ggatgtcgct gggggccaag ggcgccgccc gccctctgcc ctccga 3466

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<210> 72

<211> 1130

<212> PRT

<213> Homo sapiens

<220>

<223> Altered C-Terminus Protein (ver.2); encoded by SEQ
ID NO:71 with Intron Y ORF1

<400> 72

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
65 70 75 80

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
85 90 95

Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
 165 170 175
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
 180 185 190
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
 195 200 205
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
 210 215 220
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
 225 230 235 240
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
 245 250 255
 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
 260 265 270
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 275 280 285
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
 290 295 300
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 305 310 315 320
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 325 330 335
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
 340 345 350
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
 355 360 365
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
 370 375 380
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
 385 390 395 400
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
 405 410 415
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
 420 425 430
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
 435 440 445
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
 450 455 460

Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
 465 470 475 480
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
 675 680 685
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
 690 695 700
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
 705 710 715 720
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
 725 730 735
 Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp
 740 745 750
 Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys
 755 760 765

Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala
 770 775 780
 Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu
 785 790 795 800
 Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu
 805 810 815
 Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu
 820 825 830
 Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys
 835 840 845
 His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly
 850 855 860
 Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr
 865 870 875 880
 Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu
 885 890 895
 Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr
 900 905 910
 His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr
 915 920 925
 Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu
 930 935 940
 Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly
 945 950 955 960
 Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val
 965 970 975
 Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu
 980 985 990
 Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu
 995 1000 1005
 Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln
 1010 1015 1020
 Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu
 1025 1030 1035 1040
 Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His
 1045 1050 1055
 Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp
 1060 1065 1070

Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu
 1075 1080 1085

Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro
 1090 1095 1100

Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe Pro Val
 1105 1110 1115 1120

Ser Pro Gly Arg Gly Val Gly Leu Gly Leu
 1125 1130

<210> 73
 <211> 1045
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Altered C-Terminus Protein (ver.2); encoded by SEQ
 ID NO:71 with Intron Y ORF2 after the termination
 codon

<400> 73
 Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
 1 5 10 15

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg
 20 25 30

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
 35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
 50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
 65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
 85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
 100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
 115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg
 130 135 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
 145 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser
 165 170 175

Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala
 180 185 190
 Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
 195 200 205
 Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro
 210 215 220
 Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly
 225 230 235 240
 Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro
 245 250 255
 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro
 260 265 270
 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu
 275 280 285
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr
 290 295 300
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp
 305 310 315 320
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp
 325 330 335
 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys
 340 345 350
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val
 355 360 365
 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val
 370 375 380
 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu
 385 390 395 400
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala
 405 410 415
 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
 420 425 430
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
 435 440 445
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
 450 455 460
 Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
 465 470 475 480

Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
 485 490 495
 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
 500 505 510
 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
 515 520 525
 Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg
 530 535 540
 Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu
 545 550 555 560
 Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
 565 570 575
 Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg
 580 585 590
 Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys
 595 600 605
 Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu
 610 615 620
 Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg
 625 630 635 640
 Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr
 645 650 655
 Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp
 660 665 670
 Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr
 675 680 685
 Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val
 690 695 700
 Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro
 705 710 715 720
 Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg
 725 730 735
 Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser
 740 745 750
 Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala Val Arg
 755 760 765
 Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser
 770 775 780

Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn
 785 790 795 800
 Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val
 805 810 815
 Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe
 820 825 830
 Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn
 835 840 845
 Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly
 850 855 860
 Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys
 865 870 875 880
 Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser
 885 890 895
 Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn Arg Gly
 900 905 910
 Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu Arg
 915 920 925
 Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu Gln
 930 935 940
 Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala Tyr Arg
 945 950 955 960
 Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val Trp Lys
 965 970 975
 Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu Cys
 980 985 990
 Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu Glu Asn Ile Leu Val
 995 1000 1005
 Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro Glu Met Glu Pro Pro
 1010 1015 1020
 Arg Arg Pro Ser Gly Val Gly Ser Phe Pro Val Ser Pro Gly Arg Gly
 1025 1030 1035 1040
 Val Gly Leu Gly Leu
 1045

<210> 74
 <211> 1130
 <212> PRT
 <213> Homo sapiens

<220>

<223> Altered C-Terminus Protein (ver.2); encoded by SEQ
ID NO:71 with Intron Y ORF3

<400> 74

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Met  Pro  Arg  Ala  Pro  Arg  Cys  Arg  Ala  Val  Arg  Ser  Leu  Leu  Arg  Ser
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His  Thr  Arg  Glu  Val  Leu  Pro  Leu  Ala  Thr  Phe  Val  Arg  Arg  Leu  Gly
          20          25          30

Pro  Gln  Gly  Trp  Arg  Leu  Val  Gln  Arg  Gly  Asp  Pro  Ala  Ala  Phe  Arg
          35          40          45

Ala  Leu  Val  Ala  Gln  Cys  Leu  Val  Cys  Val  Pro  Trp  Asp  Ala  Arg  Pro
          50          55          60

Pro  Pro  Ala  Ala  Pro  Ser  Phe  Arg  Gln  Val  Pro  Pro  Arg  Gly  Arg  Arg
          65          70          75          80

Pro  Ala  Gly  Val  Glu  Gly  Gly  Arg  Gly  Glu  Pro  Ala  Thr  Cys  Gly  Glu
          85          90          95

Gln  Arg  Arg  Arg  Leu  Arg  Ala  Leu  Pro  Pro  Gln  Val  Ser  Cys  Leu  Lys
          100          105          110

Glu  Leu  Val  Ala  Arg  Val  Leu  Gln  Arg  Leu  Cys  Glu  Arg  Gly  Ala  Lys
          115          120          125

Asn  Val  Leu  Ala  Phe  Gly  Phe  Ala  Leu  Leu  Asp  Gly  Ala  Arg  Gly  Gly
          130          135          140

Pro  Pro  Glu  Ala  Phe  Thr  Thr  Ser  Val  Arg  Ser  Tyr  Leu  Pro  Asn  Thr
          145          150          155          160

Val  Thr  Asp  Ala  Leu  Arg  Gly  Ser  Gly  Ala  Trp  Gly  Leu  Leu  Leu  Arg
          165          170          175

Arg  Val  Gly  Asp  Asp  Val  Leu  Val  His  Leu  Leu  Ala  Arg  Cys  Ala  Leu
          180          185          190

Phe  Val  Leu  Val  Ala  Pro  Ser  Cys  Ala  Tyr  Gln  Val  Cys  Gly  Pro  Pro
          195          200          205

Leu  Tyr  Gln  Leu  Gly  Ala  Ala  Thr  Gln  Ala  Arg  Pro  Pro  Pro  His  Ala
          210          215          220

Ser  Gly  Pro  Arg  Arg  Arg  Leu  Gly  Cys  Glu  Arg  Ala  Trp  Asn  His  Ser
          225          230          235          240

Val  Arg  Glu  Ala  Gly  Val  Pro  Leu  Gly  Leu  Pro  Ala  Pro  Gly  Ala  Arg
          245          250          255

Arg  Arg  Gly  Gly  Ser  Ala  Ser  Arg  Ser  Leu  Pro  Leu  Pro  Lys  Arg  Pro
          260          265          270

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Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 275 280 285
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
 290 295 300
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 305 310 315 320
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 325 330 335
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
 340 345 350
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
 355 360 365
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
 370 375 380
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
 385 390 395 400
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
 405 410 415
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
 420 425 430
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
 435 440 445
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
 450 455 460
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
 465 470 475 480
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
 675 680 685
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
 690 695 700
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
 705 710 715 720
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
 725 730 735
 Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp
 740 745 750
 Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys
 755 760 765
 Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala
 770 775 780
 Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu
 785 790 795 800
 Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu
 805 810 815
 Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu
 820 825 830
 Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys
 835 840 845
 His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly
 850 855 860
 Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr
 865 870 875 880

Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu
 885 890 895
 Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr
 900 905 910
 His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr
 915 920 925
 Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu
 930 935 940
 Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly
 945 950 955 960
 Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val
 965 970 975
 Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu
 980 985 990
 Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu
 995 1000 1005
 Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln
 1010 1015 1020
 Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu
 1025 1030 1035 1040
 Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His
 1045 1050 1055
 Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp
 1060 1065 1070
 Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu
 1075 1080 1085
 Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro
 1090 1095 1100
 Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe Pro Val
 1105 1110 1115 1120
 Ser Pro Gly Arg Gly Val Gly Leu Gly Leu
 1125 1130

<210> 75
 <211> 4022
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Protein Lacking Motif A (ver.2); with Introns Y
 and Beta

<400> 75

atgccgcgcg	ctccccgctg	ccgagccgtg	cgctccctgc	tgcgcagcca	ctaccgcgag	60
gtgctgccgc	tggccacgtt	cgtgcggcgc	ctggggcccc	agggctggcg	gctgggtgcag	120
cgcggggacc	cggcggcttt	ccgcgcgctg	gtggcccagt	gcctgggtgtg	cgtgccctgg	180
gacgcacggc	cgccccccgc	cgccccctcc	ttccgccagg	tgggcctccc	cggggctcggc	240
gtccggctgg	ggttgagggc	ggccgggggg	aaccagcgac	atgcggagag	cagcgcaggc	300
gactcagggc	gcttcccccg	caggtgtcct	gcctgaagga	gctgggtggc	cgagtgtctg	360
agaggctgtg	cgagcgcggc	gcgaagaacg	tgctggcctt	cggcttcgcg	ctgctggacg	420
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tcctgctcaa gctgactcga caccgtgtca cctacgtgcc actcctgggg tcaactcagga 3360
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ga 4022

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<210> 76
<211> 1154
<212> PRT
<213> Homo sapiens

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<220>
<223> Protein Lacking Motif A (ver.2); encoded by SEQ ID
      NO:75 with Intron Y ORF1

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<400> 76
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His  Thr  Arg  Glu  Val  Leu  Pro  Leu  Ala  Thr  Phe  Val  Arg  Arg  Leu  Gly
      20              25              30

Pro  Gln  Gly  Trp  Arg  Leu  Val  Gln  Arg  Gly  Asp  Pro  Ala  Ala  Phe  Arg
      35              40              45

Ala  Leu  Val  Ala  Gln  Cys  Leu  Val  Cys  Val  Pro  Trp  Asp  Ala  Arg  Pro
      50              55              60

Pro  Pro  Ala  Ala  Pro  Ser  Phe  Arg  Gln  Val  Gly  Leu  Pro  Gly  Val  Gly
      65              70              75              80

Val  Arg  Leu  Gly  Leu  Arg  Ala  Ala  Gly  Gly  Asn  Gln  Arg  His  Ala  Glu
      85              90              95

Ser  Ser  Ala  Gly  Asp  Ser  Gly  Arg  Phe  Pro  Arg  Arg  Ser  Cys  Leu  Lys
      100              105              110

Glu  Leu  Val  Ala  Arg  Val  Leu  Gln  Arg  Leu  Cys  Glu  Arg  Gly  Ala  Lys
      115              120              125

Asn  Val  Leu  Ala  Phe  Gly  Phe  Ala  Leu  Leu  Asp  Gly  Ala  Arg  Gly  Gly
      130              135              140

Pro  Pro  Glu  Ala  Phe  Thr  Thr  Ser  Val  Arg  Ser  Tyr  Leu  Pro  Asn  Thr
      145              150              155              160

Val  Thr  Asp  Ala  Leu  Arg  Gly  Ser  Gly  Ala  Trp  Gly  Leu  Leu  Leu  Arg
      165              170              175

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Arg	Val	Gly	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu	180	185	190
Phe	Val	Leu	Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro	195	200	205
Leu	Tyr	Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala	210	215	220
Ser	Gly	Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser	225	230	235
Val	Arg	Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg	245	250	255
Arg	Arg	Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro	260	265	270
Arg	Arg	Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly	275	280	285
Ser	Trp	Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe	290	295	300
Cys	Val	Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu	305	310	315
Gly	Ala	Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln	325	330	335
His	His	Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp	340	345	350
Thr	Pro	Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser	355	360	365
Ser	Gly	Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu	370	375	380
Arg	Pro	Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu	385	390	395
Gly	Ser	Arg	Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu	405	410	415
Pro	Gln	Arg	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly	420	425	430
Asn	His	Ala	Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro	435	440	445
Leu	Arg	Ala	Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys	450	455	460
Pro	Gln	Gly	Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg	465	470	475
																		480

Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
 675 680 685
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
 690 695 700
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
 705 710 715 720
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
 725 730 735
 Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala
 740 745 750
 Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val
 755 760 765
 Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His
 770 775 780

Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala
 785 790 795 800
 His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln
 805 810 815
 Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu
 820 825 830
 Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val
 835 840 845
 Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys
 850 855 860
 Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg
 865 870 875 880
 Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr
 885 890 895
 Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly
 900 905 910
 Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn
 915 920 925
 Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met
 930 935 940
 Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg
 945 950 955 960
 Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile
 965 970 975
 Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met
 980 985 990
 Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe
 995 1000 1005
 Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr
 1010 1015 1020
 Lys Ile Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln
 1025 1030 1035 1040
 Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg
 1045 1050 1055
 Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys
 1060 1065 1070
 Asn Ala Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro
 1075 1080 1085

Ser Glu Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu
 1090 1095 1100

Thr Arg His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr
 1105 1110 1115 1120

Ala Gln Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala
 1125 1130 1135

Leu Glu Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile
 1140 1145 1150

Leu Asp

<210> 77
 <211> 1069
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Protein Lacking Motif A (ver.2); encoded by SEQ ID
 NO:75 with Intron Y ORF2 after the termination
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<400> 77
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Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg
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Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
 35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
 50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
 65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
 85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
 100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
 115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg
 130 135 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
 145 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser
 165 170 175
 Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala
 180 185 190
 Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
 195 200 205
 Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro
 210 215 220
 Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly
 225 230 235 240
 Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro
 245 250 255
 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro
 260 265 270
 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu
 275 280 285
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr
 290 295 300
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp
 305 310 315 320
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp
 325 330 335
 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys
 340 345 350
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val
 355 360 365
 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val
 370 375 380
 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu
 385 390 395 400
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala
 405 410 415
 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
 420 425 430
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
 435 440 445
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
 450 455 460

Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val	Gly	Cys	Val	Pro	Ala	465	470	475	480
Ala	Glu	His	Arg	Leu	Arg	Glu	Glu	Ile	Leu	Ala	Lys	Phe	Leu	His	Trp	485	490	495	
Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg	Ser	Phe	Phe	Tyr	Val	500	505	510	
Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe	Phe	Tyr	Arg	Lys	Ser	515	520	525	
Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile	Arg	Gln	His	Leu	Lys	Arg	530	535	540	
Val	Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu	Val	Arg	Gln	His	Arg	Glu	545	550	555	560
Ala	Arg	Pro	Ala	Leu	Leu	Thr	Ser	Arg	Leu	Arg	Phe	Ile	Pro	Lys	Pro	565	570	575	
Asp	Gly	Leu	Arg	Pro	Ile	Val	Asn	Met	Asp	Tyr	Val	Val	Gly	Ala	Arg	580	585	590	
Thr	Phe	Arg	Arg	Glu	Lys	Arg	Ala	Glu	Arg	Leu	Thr	Ser	Arg	Val	Lys	595	600	605	
Ala	Leu	Phe	Ser	Val	Leu	Asn	Tyr	Glu	Arg	Ala	Arg	Arg	Pro	Gly	Leu	610	615	620	
Leu	Gly	Ala	Ser	Val	Leu	Gly	Leu	Asp	Asp	Ile	His	Arg	Ala	Trp	Arg	625	630	635	640
Thr	Phe	Val	Leu	Arg	Val	Arg	Ala	Gln	Asp	Pro	Pro	Pro	Glu	Leu	Tyr	645	650	655	
Phe	Val	Lys	Asp	Arg	Leu	Thr	Glu	Val	Ile	Ala	Ser	Ile	Ile	Lys	Pro	660	665	670	
Gln	Asn	Thr	Tyr	Cys	Val	Arg	Arg	Tyr	Ala	Val	Val	Gln	Lys	Ala	Ala	675	680	685	
His	Gly	His	Val	Arg	Lys	Ala	Phe	Lys	Ser	His	Val	Ser	Thr	Leu	Thr	690	695	700	
Asp	Leu	Gln	Pro	Tyr	Met	Arg	Gln	Phe	Val	Ala	His	Leu	Gln	Glu	Thr	705	710	715	720
Ser	Pro	Leu	Arg	Asp	Ala	Val	Val	Ile	Glu	Gln	Ser	Ser	Ser	Leu	Asn	725	730	735	
Glu	Ala	Ser	Ser	Gly	Leu	Phe	Asp	Val	Phe	Leu	Arg	Phe	Met	Cys	His	740	745	750	
His	Ala	Val	Arg	Ile	Arg	Gly	Lys	Ser	Tyr	Val	Gln	Cys	Gln	Gly	Ile	755	760	765	

Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly
 770 775 780
 Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu
 785 790 795 800
 Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His
 805 810 815
 Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly
 820 825 830
 Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp
 835 840 845
 Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu
 850 855 860
 Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln
 865 870 875 880
 Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr
 885 890 895
 Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe
 900 905 910
 Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val
 915 920 925
 Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu
 930 935 940
 Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln
 945 950 955 960
 Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr
 965 970 975
 Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser
 980 985 990
 Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln
 995 1000 1005
 Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val
 1010 1015 1020
 Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu
 1025 1030 1035 1040
 Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala
 1045 1050 1055
 Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 1060 1065

<210> 78
 <211> 1154
 <212> PRT
 <213> Homo sapiens

<220>

<223> Protein Lacking Motif A (ver.2); encoded by SEQ ID
 NO:75 with Intron Y ORF3

<400> 78

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          20              25              30

Pro  Gln Gly  Trp  Arg  Leu  Val  Gln Arg  Gly  Asp  Pro  Ala  Ala  Phe  Arg
          35              40              45

Ala  Leu Val  Ala  Gln  Cys  Leu  Val  Cys  Val  Pro  Trp  Asp  Ala  Arg  Pro
          50              55              60

Pro  Pro Ala  Ala  Pro  Ser  Phe  Arg  Gln  Val  Pro  Pro  Arg  Gly  Arg  Arg
 65              70              75              80

Pro  Ala Gly  Val  Glu  Gly  Gly  Arg  Gly  Glu  Pro  Ala  Thr  Cys  Gly  Glu
          85              90              95

Gln  Arg Arg  Arg  Leu  Arg  Ala  Leu  Pro  Gln  Val  Ser  Cys  Leu  Lys
          100             105             110

Glu  Leu Val  Ala  Arg  Val  Leu  Gln  Arg  Leu  Cys  Glu  Arg  Gly  Ala  Lys
          115             120             125

Asn  Val  Leu  Ala  Phe  Gly  Phe  Ala  Leu  Leu  Asp  Gly  Ala  Arg  Gly  Gly
          130             135             140

Pro  Pro Glu  Ala  Phe  Thr  Thr  Ser  Val  Arg  Ser  Tyr  Leu  Pro  Asn  Thr
145              150             155             160

Val  Thr Asp  Ala  Leu  Arg  Gly  Ser  Gly  Ala  Trp  Gly  Leu  Leu  Leu  Arg
          165             170             175

Arg  Val Gly  Asp  Asp  Val  Leu  Val  His  Leu  Leu  Ala  Arg  Cys  Ala  Leu
          180             185             190

Phe  Val  Leu  Val  Ala  Pro  Ser  Cys  Ala  Tyr  Gln  Val  Cys  Gly  Pro  Pro
          195             200             205

Leu  Tyr Gln  Leu  Gly  Ala  Ala  Thr  Gln  Ala  Arg  Pro  Pro  Pro  His  Ala
          210             215             220

Ser  Gly  Pro  Arg  Arg  Arg  Leu  Gly  Cys  Glu  Arg  Ala  Trp  Asn  His  Ser
225              230             235             240

Val  Arg  Glu  Ala  Gly  Val  Pro  Leu  Gly  Leu  Pro  Ala  Pro  Gly  Ala  Arg

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			245					250					255		
Arg	Arg	Gly	Gly 260	Ser	Ala	Ser	Arg	Ser 265	Leu	Pro	Leu	Pro	Lys 270	Arg	Pro
Arg	Arg	Gly 275	Ala	Ala	Pro	Glu	Pro 280	Glu	Arg	Thr	Pro	Val 285	Gly	Gln	Gly
Ser	Trp 290	Ala	His	Pro	Gly	Arg 295	Thr	Arg	Gly	Pro	Ser 300	Asp	Arg	Gly	Phe
Cys 305	Val	Val	Ser	Pro	Ala 310	Arg	Pro	Ala	Glu	Glu 315	Ala	Thr	Ser	Leu	Glu 320
Gly	Ala	Leu	Ser	Gly 325	Thr	Arg	His	Ser	His 330	Pro	Ser	Val	Gly	Arg 335	Gln
His	His	Ala	Gly 340	Pro	Pro	Ser	Thr	Ser 345	Arg	Pro	Pro	Arg	Pro 350	Trp	Asp
Thr	Pro	Cys 355	Pro	Pro	Val	Tyr	Ala 360	Glu	Thr	Lys	His	Phe 365	Leu	Tyr	Ser
Ser	Gly 370	Asp	Lys	Glu	Gln	Leu 375	Arg	Pro	Ser	Phe	Leu 380	Leu	Ser	Ser	Leu
Arg 385	Pro	Ser	Leu	Thr	Gly 390	Ala	Arg	Arg	Leu	Val 395	Glu	Thr	Ile	Phe	Leu 400
Gly	Ser	Arg	Pro	Trp 405	Met	Pro	Gly	Thr	Pro 410	Arg	Arg	Leu	Pro	Arg 415	Leu
Pro	Gln	Arg	Tyr 420	Trp	Gln	Met	Arg	Pro 425	Leu	Phe	Leu	Glu	Leu 430	Leu	Gly
Asn	His	Ala 435	Gln	Cys	Pro	Tyr	Gly 440	Val	Leu	Leu	Lys	Thr 445	His	Cys	Pro
Leu	Arg	Ala	Ala	Val	Thr	Pro 455	Ala	Ala	Gly	Val	Cys 460	Ala	Arg	Glu	Lys
Pro 465	Gln	Gly	Ser	Val	Ala 470	Ala	Pro	Glu	Glu	Glu 475	Asp	Thr	Asp	Pro	Arg 480
Arg	Leu	Val	Gln	Leu 485	Leu	Arg	Gln	His	Ser 490	Ser	Pro	Trp	Gln	Val 495	Tyr
Gly	Phe	Val	Arg 500	Ala	Cys	Leu	Arg	Arg 505	Leu	Val	Pro	Pro	Gly 510	Leu	Trp
Gly	Ser	Arg 515	His	Asn	Glu	Arg	Arg 520	Phe	Leu	Arg	Asn	Thr 525	Lys	Lys	Phe
Ile	Ser 530	Leu	Gly	Lys	His	Ala 535	Lys	Leu	Ser	Leu	Gln 540	Glu	Leu	Thr	Trp
Lys	Met	Ser	Val	Arg	Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val

545		550		555		560
Gly Cys Val Pro	Ala Ala Glu His Arg	Leu Arg Glu Glu Ile	Leu Ala			
	565	570	575			
Lys Phe Leu His Trp	Leu Met Ser Val Tyr	Val Val Glu Leu	Leu Arg			
	580	585	590			
Ser Phe Phe Tyr Val Thr	Glu Thr Thr Phe Gln Lys	Asn Arg Leu Phe				
	595	600	605			
Phe Tyr Arg Lys Ser Val	Trp Ser Lys Leu Gln Ser	Ile Gly Ile Arg				
	610	615	620			
Gln His Leu Lys Arg Val	Gln Leu Arg Glu Leu Ser	Glu Ala Glu Val				
	625	630	635			640
Arg Gln His Arg Glu Ala	Arg Pro Ala Leu Leu Thr	Ser Arg Leu Arg				
	645	650	655			
Phe Ile Pro Lys Pro Asp	Gly Leu Arg Pro Ile Val	Asn Met Asp Tyr				
	660	665	670			
Val Val Gly Ala Arg Thr	Phe Arg Arg Glu Lys Arg	Ala Glu Arg Leu				
	675	680	685			
Thr Ser Arg Val Lys Ala	Leu Phe Ser Val Leu Asn	Tyr Glu Arg Ala				
	690	695	700			
Arg Arg Pro Gly Leu Leu	Gly Ala Ser Val Leu Gly	Leu Asp Asp Ile				
	705	710	715			720
His Arg Ala Trp Arg Thr	Phe Val Leu Arg Val Arg	Ala Gln Asp Pro				
	725	730	735			
Pro Pro Glu Leu Tyr Phe	Val Lys Asp Arg Leu Thr	Glu Val Ile Ala				
	740	745	750			
Ser Ile Ile Lys Pro Gln	Asn Thr Tyr Cys Val Arg	Arg Tyr Ala Val				
	755	760	765			
Val Gln Lys Ala Ala His	Gly His Val Arg Lys Ala	Phe Lys Ser His				
	770	775	780			
Val Ser Thr Leu Thr Asp	Leu Gln Pro Tyr Met Arg	Gln Phe Val Ala				
	785	790	795			800
His Leu Gln Glu Thr Ser	Pro Leu Arg Asp Ala Val	Val Ile Glu Gln				
	805	810	815			
Ser Ser Ser Leu Asn Glu	Ala Ser Ser Gly Leu Phe	Asp Val Phe Leu				
	820	825	830			
Arg Phe Met Cys His His	Ala Val Arg Ile Arg Gly	Lys Ser Tyr Val				
	835	840	845			
Gln Cys Gln Gly Ile Pro	Gln Gly Ser Ile Leu Ser	Thr Leu Leu Cys				

850	855	860
Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg 865 870 875 880		
Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr 885 890 895		
Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly 900 905 910		
Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn 915 920 925		
Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met 930 935 940		
Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg 945 950 955 960		
Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile 965 970 975		
Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met 980 985 990		
Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe 995 1000 1005		
Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr 1010 1015 1020		
Lys Ile Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln 1025 1030 1035 1040		
Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg 1045 1050 1055		
Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys 1060 1065 1070		
Asn Ala Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro 1075 1080 1085		
Ser Glu Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu 1090 1095 1100		
Thr Arg His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr 1105 1110 1115 1120		
Ala Gln Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala 1125 1130 1135		
Leu Glu Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile 1140 1145 1150		
Leu Asp		

<210> 79
 <211> 3137
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Truncated Protein Lacking Motif A (ver.2); with
 Introns Y, Beta and 2

<400> 79
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 gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctgggtgag 120
 cgcggggacc cggcggcttt ccgcgcgctg gtggcccagt gcctgggtgt cgtgccctgg 180
 gacgcacggc cgccccccgc cgccccctcc ttccgccagg tgggcctccc cggggtcggc 240
 gtccggctgg ggttaggggc ggccgggggg aaccagcgac atgcggagag cagcgcaggc 300
 gactcagggc gcttcccccg caggtgtcct gcctgaagga gctgggtggc cgagtgtctg 360
 agaggctgtg cgagcgcggc gcgaagaacg tgcctggcctt cggtctcgcg ctgctggacg 420
 gggcccgcgg gggccccccc gaggccttca ccaccagcgt gcgcagctac ctgcccaaca 480
 cgggtgaccga cgcactgcgg gggagcgggg cgtgggggct gctgctgcgc cgctggggcg 540
 acgacgtgct ggttcacctg ctggcacgct gcgcgctctt tgtgctggtg gctcccagct 600
 gcgctacca ggtgtgcggg ccgcgcgctgt accagctcgg cgctgccact caggcccggc 660
 ccccgccaca cgctagtggg ccccgaaggc gtctgggatg cgaacgggac tggaaaccata 720
 gcgtcaggga ggccggggtc cccctggggc tgccagcccc ggggtgcgag aggcgcgggg 780
 gcagtgccag ccgaagtctg ccgttgccca agaggcccag gcgtggcgct gccctgagc 840
 cggagcggac gcccgttggg caggggtcct gggcccaccc gggcaggacg cgtggaccga 900
 gtgaccgtgg tttctgtgtg gtgtcacctg ccagaccgcg cgaagaagcc acctctttgg 960
 aggggtgcgt ctctggcacg cgccactccc acccatccgt gggccgccag caccacgcgg 1020
 gccccccatc cacatcgcgg ccaccacgtc cctgggacac gccttgtccc ccggtgtacg 1080
 ccgagacca gcacttcttc tactcctcag gcgacaagga gcagtgcgg cctccttcc 1140
 tactcagctc tctgaggccc agcctgactg gcgctcgag gctcgtggag accatctttc 1200
 tgggttccag gccctggatg ccagggactc cccgcagggt gccccgcctg cccagcgct 1260
 actggcaaat gcggcccctg tttctggagc tgcttgggaa ccacgcgcag tgcccctacg 1320
 ggggtgtcct caagacgcac tgcccgtgc gagctgcgt caccacagca gccggtgtct 1380
 gtgcccggga gaagccccag ggctctgtgg cggccccga ggaggaggac acagaccccc 1440
 gtcgcctggt gcagctgtc cgccagcaca gcagcccctg gcagggtgtac ggcttcgtgc 1500
 gggcctgcct gcgcgggctg gtgccccag gcctctgggg ctccaggcac aacgaacgcc 1560
 gcttctcag gaacaccaag aagttcatct cctggggaa gcatgccaag ctctcgctgc 1620
 aggagctgac gtggaagatg agcgtgcggg actgcgctt gctgcgcagg agcccaggg 1680
 ttggctgtgt tccggccgca gagcacgctc tgctgagga gatcctggcc aagttcctgc 1740
 actggctgat gagtgtgtac gtcgtcgagc tgctcaggtc tttcttttat gtcacggaga 1800
 ccacgtttca aaagaacagg ctctttttct accggaagag tgtctggagc aagttgcaa 1860
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 tcaggcagca tcgggaagcc aggccgcgcc tgctgacgtc cagactccgc ttcacccca 1980
 agcctgacgg gctgcggccg attgtgaaca tggactacgt cgtgggagcc agaacgttcc 2040
 gcagagaaa gagggccgag cgtctcacct cgaggggtga ggcactgttc agcgtgtca 2100
 actacagcg ggccgcgcgc cccggcctcc tgggcgcctc tgtgtggggc ctggagata 2160
 tccacagggc ctggcgacc cttcgtgtgc gtgtgcgggc ccaggaccgc ccgctgagc 2220
 tgtactttgt caaggacagg ctacagggag tcatcgccag catcatcaa cccagaaca 2280
 cgtactgct gcgtcggtat gccgtggtcc agaaggccgc ccatgggcac gtccgcaagg 2340
 ccttcaagag ccacgtctct accttgacag acctccagcc gtacatgcga cagttcgtgg 2400
 ctcacctgca ggagaccagc ccgctgaggg atgccgtcgt catcgagcag agctcctccc 2460
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 tgcgcacag gggcaagtcc tacgtccagt gccaggggat cccgcagggc tccatcctct 2580
 ccacgctgct ctgcagcctg tgctacggcg acatggagaa caagctgttt gcggggattc 2640

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ggcgggacgg gctgctcctg cgtttggtgg atgatttctt gttggtgaca cctcacctca 2700
cccacgcgaa aaccttcctc aggaccctgg tccgaggtgt ccctgagtat ggctgcgtgg 2760
tgaacttgcg gaagacagtg gtgaacttcc ctgtagaaga cgaggccctg ggtggcacgg 2820
cttttgttca gatgccggcc cacggcctat tcccctggtg cggcctgctg ctggataccc 2880
ggaccctgga ggtgcagagc gactactcca ggtgagcgca cctggccgga agtggagcct 2940
gtgcccggct ggggcaggtg ctgctgcagg gccgttgctg ccacctctgc ttccgtgtgg 3000
ggcaggcgac tgccaatccc aaagggtcag atgccacagg gtgcccctcg tcccatctgg 3060
ggctgagcac aaatgcatct ttctgtggga gtgagggtgc ctcacaacgg gagcagtttt 3120
ctgtgctatt ttggttaa                                     3137

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<210> 80
<211> 970
<212> PRT
<213> Homo sapiens

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<220>
<223> Truncated Protein lacking Motif A (ver.2); encoded
      by SEQ ID NO:79 with Intron Y ORF1

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Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
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His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
  20              25              30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
  35              40              45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
  50              55              60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
  65              70              75              80

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
  85              90              95

Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
 100              105              110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
 115              120              125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
 130              135              140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
 145              150              155              160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
 165              170              175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
 180              185              190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro

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195					200					205					
Leu	Tyr	Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala
210					215					220					
Ser	Gly	Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser
225					230					235					240
Val	Arg	Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg
				245					250					255	
Arg	Arg	Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro
			260					265					270		
Arg	Arg	Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly
			275				280					285			
Ser	Trp	Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe
	290					295					300				
Cys	Val	Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu
305					310					315					320
Gly	Ala	Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln
				325					330					335	
His	His	Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp
			340					345					350		
Thr	Pro	Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser
		355					360					365			
Ser	Gly	Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu
	370					375					380				
Arg	Pro	Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu
385					390					395					400
Gly	Ser	Arg	Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu
				405					410					415	
Pro	Gln	Arg	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly
			420					425					430		
Asn	His	Ala	Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro
		435					440					445			
Leu	Arg	Ala	Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys
	450					455					460				
Pro	Gln	Gly	Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg
465					470					475					480
Arg	Leu	Val	Gln	Leu	Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	Tyr
				485					490					495	
Gly	Phe	Val	Arg	Ala	Cys	Leu	Arg	Arg	Leu	Val	Pro	Pro	Gly	Leu	Trp

500					505					510					
Gly	Ser	Arg	His	Asn	Glu	Arg	Arg	Phe	Leu	Arg	Asn	Thr	Lys	Lys	Phe
		515					520					525			
Ile	Ser	Leu	Gly	Lys	His	Ala	Lys	Leu	Ser	Leu	Gln	Glu	Leu	Thr	Trp
	530					535					540				
Lys	Met	Ser	Val	Arg	Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val
545					550					555					560
Gly	Cys	Val	Pro	Ala	Ala	Glu	His	Arg	Leu	Arg	Glu	Glu	Ile	Leu	Ala
				565					570					575	
Lys	Phe	Leu	His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg
			580					585					590		
Ser	Phe	Phe	Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe
		595					600					605			
Phe	Tyr	Arg	Lys	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile	Arg
	610					615					620				
Gln	His	Leu	Lys	Arg	Val	Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu	Val
625					630					635					640
Arg	Gln	His	Arg	Glu	Ala	Arg	Pro	Ala	Leu	Leu	Thr	Ser	Arg	Leu	Arg
				645					650					655	
Phe	Ile	Pro	Lys	Pro	Asp	Gly	Leu	Arg	Pro	Ile	Val	Asn	Met	Asp	Tyr
			660					665				670			
Val	Val	Gly	Ala	Arg	Thr	Phe	Arg	Arg	Glu	Lys	Arg	Ala	Glu	Arg	Leu
		675					680					685			
Thr	Ser	Arg	Val	Lys	Ala	Leu	Phe	Ser	Val	Leu	Asn	Tyr	Glu	Arg	Ala
	690					695					700				
Arg	Arg	Pro	Gly	Leu	Leu	Gly	Ala	Ser	Val	Leu	Gly	Leu	Asp	Asp	Ile
705					710					715					720
His	Arg	Ala	Trp	Arg	Thr	Phe	Val	Leu	Arg	Val	Arg	Ala	Gln	Asp	Pro
				725					730					735	
Pro	Pro	Glu	Leu	Tyr	Phe	Val	Lys	Asp	Arg	Leu	Thr	Glu	Val	Ile	Ala
			740					745					750		
Ser	Ile	Ile	Lys	Pro	Gln	Asn	Thr	Tyr	Cys	Val	Arg	Arg	Tyr	Ala	Val
		755					760					765			
Val	Gln	Lys	Ala	Ala	His	Gly	His	Val	Arg	Lys	Ala	Phe	Lys	Ser	His
	770					775					780				
Val	Ser	Thr	Leu	Thr	Asp	Leu	Gln	Pro	Tyr	Met	Arg	Gln	Phe	Val	Ala
785					790					795					800
His	Leu	Gln	Glu	Thr	Ser	Pro	Leu	Arg	Asp	Ala	Val	Val	Ile	Glu	Gln

805					810					815					
Ser	Ser	Ser	Leu	Asn	Glu	Ala	Ser	Ser	Gly	Leu	Phe	Asp	Val	Phe	Leu
			820					825					830		
Arg	Phe	Met	Cys	His	His	Ala	Val	Arg	Ile	Arg	Gly	Lys	Ser	Tyr	Val
		835					840					845			
Gln	Cys	Gln	Gly	Ile	Pro	Gln	Gly	Ser	Ile	Leu	Ser	Thr	Leu	Leu	Cys
	850					855					860				
Ser	Leu	Cys	Tyr	Gly	Asp	Met	Glu	Asn	Lys	Leu	Phe	Ala	Gly	Ile	Arg
865					870					875					880
Arg	Asp	Gly	Leu	Leu	Leu	Arg	Leu	Val	Asp	Asp	Phe	Leu	Leu	Val	Thr
			885						890					895	
Pro	His	Leu	Thr	His	Ala	Lys	Thr	Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly
		900						905					910		
Val	Pro	Glu	Tyr	Gly	Cys	Val	Val	Asn	Leu	Arg	Lys	Thr	Val	Val	Asn
		915					920					925			
Phe	Pro	Val	Glu	Asp	Glu	Ala	Leu	Gly	Gly	Thr	Ala	Phe	Val	Gln	Met
	930					935					940				
Pro	Ala	His	Gly	Leu	Phe	Pro	Trp	Cys	Gly	Leu	Leu	Leu	Asp	Thr	Arg
945					950					955					960
Thr	Leu	Glu	Val	Gln	Ser	Asp	Tyr	Ser	Arg						
			965						970						

<210> 81
 <211> 885
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Truncated Protein lacking Motif A (ver.2); encoded
 by SEQ ID NO:79 with Intron Y ORF2 after the
 termination codon

<400> 81															
Gly	Arg	Pro	Gly	Gly	Thr	Ser	Asp	Met	Arg	Arg	Ala	Ala	Gln	Ala	Thr
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Gln	Gly	Ala	Ser	Pro	Ala	Gly	Ser	Cys	Leu	Lys	Glu	Leu	Val	Ala	Arg
			20					25					30		
Val	Leu	Gln	Arg	Leu	Cys	Glu	Arg	Gly	Ala	Lys	Asn	Val	Leu	Ala	Phe
		35					40					45			
Gly	Phe	Ala	Leu	Leu	Asp	Gly	Ala	Arg	Gly	Gly	Pro	Pro	Glu	Ala	Phe
	50					55					60				
Thr	Thr	Ser	Val	Arg	Ser	Tyr	Leu	Pro	Asn	Thr	Val	Thr	Asp	Ala	Leu

65					70						75				80
Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu	Leu	Arg	Arg	Val	Gly	Asp	Asp
				85					90					95	
Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu	Phe	Val	Leu	Val	Ala
			100					105					110		
Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro	Leu	Tyr	Gln	Leu	Gly
		115					120					125			
Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala	Ser	Gly	Pro	Arg	Arg
		130				135					140				
Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser	Val	Arg	Glu	Ala	Gly
145					150					155					160
Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg	Arg	Arg	Gly	Gly	Ser
				165					170					175	
Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro	Arg	Arg	Gly	Ala	Ala
			180					185					190		
Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly	Ser	Trp	Ala	His	Pro
		195					200					205			
Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe	Cys	Val	Val	Ser	Pro
	210					215					220				
Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu	Gly	Ala	Leu	Ser	Gly
225					230					235					240
Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln	His	His	Ala	Gly	Pro
				245					250					255	
Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp	Thr	Pro	Cys	Pro	Pro
			260					265					270		
Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser	Ser	Gly	Asp	Lys	Glu
		275					280					285			
Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu	Arg	Pro	Ser	Leu	Thr
	290					295					300				
Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu	Gly	Ser	Arg	Pro	Trp
305					310					315					320
Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu	Pro	Gln	Arg	Tyr	Trp
				325					330					335	
Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly	Asn	His	Ala	Gln	Cys
			340					345					350		
Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro	Leu	Arg	Ala	Ala	Val
		355					360					365			
Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys	Pro	Gln	Gly	Ser	Val

370		375		380
Ala 385	Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu	390	395	400
Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala	405	410	415	
Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn	420	425	430	
Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys	435	440	445	
His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg	450	455	460	
Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala	465	470	475	480
Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp	485	490	495	
Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val	500	505	510	
Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser	515	520	525	
Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg	530	535	540	
Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu	545	550	555	560
Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro	565	570	575	
Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg	580	585	590	
Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys	595	600	605	
Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu	610	615	620	
Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg	625	630	635	640
Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr	645	650	655	
Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro	660	665	670	
Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala				

675					680					685					
His	Gly	His	Val	Arg	Lys	Ala	Phe	Lys	Ser	His	Val	Ser	Thr	Leu	Thr
690						695					700				
Asp	Leu	Gln	Pro	Tyr	Met	Arg	Gln	Phe	Val	Ala	His	Leu	Gln	Glu	Thr
705					710					715					720
Ser	Pro	Leu	Arg	Asp	Ala	Val	Val	Ile	Glu	Gln	Ser	Ser	Ser	Leu	Asn
				725					730					735	
Glu	Ala	Ser	Ser	Gly	Leu	Phe	Asp	Val	Phe	Leu	Arg	Phe	Met	Cys	His
				740				745					750		
His	Ala	Val	Arg	Ile	Arg	Gly	Lys	Ser	Tyr	Val	Gln	Cys	Gln	Gly	Ile
		755					760					765			
Pro	Gln	Gly	Ser	Ile	Leu	Ser	Thr	Leu	Leu	Cys	Ser	Leu	Cys	Tyr	Gly
	770					775					780				
Asp	Met	Glu	Asn	Lys	Leu	Phe	Ala	Gly	Ile	Arg	Arg	Asp	Gly	Leu	Leu
785					790					795					800
Leu	Arg	Leu	Val	Asp	Asp	Phe	Leu	Leu	Val	Thr	Pro	His	Leu	Thr	His
				805					810					815	
Ala	Lys	Thr	Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly	Val	Pro	Glu	Tyr	Gly
			820					825					830		
Cys	Val	Val	Asn	Leu	Arg	Lys	Thr	Val	Val	Asn	Phe	Pro	Val	Glu	Asp
		835					840					845			
Glu	Ala	Leu	Gly	Gly	Thr	Ala	Phe	Val	Gln	Met	Pro	Ala	His	Gly	Leu
	850					855					860				
Phe	Pro	Trp	Cys	Gly	Leu	Leu	Leu	Asp	Thr	Arg	Thr	Leu	Glu	Val	Gln
865					870					875					880
Ser	Asp	Tyr	Ser	Arg											
				885											

<210> 82

<211> 970

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein lacking Motif A (ver.2); encoded
by SEQ ID NO:79 with Intron Y ORF3

<400> 82

Met	Pro	Arg	Ala	Pro	Arg	Cys	Arg	Ala	Val	Arg	Ser	Leu	Leu	Arg	Ser
1				5					10					15	

His	Thr	Arg	Glu	Val	Leu	Pro	Leu	Ala	Thr	Phe	Val	Arg	Arg	Leu	Gly
			20					25					30		

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
 65 70 75 80
 Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu
 85 90 95
 Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys
 100 105 110
 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
 115 120 125
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
 130 135 140
 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
 145 150 155 160
 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
 165 170 175
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
 180 185 190
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
 195 200 205
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
 210 215 220
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
 225 230 235 240
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
 245 250 255
 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
 260 265 270
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 275 280 285
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
 290 295 300
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 305 310 315 320
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 325 330 335

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
 340 345 350
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
 355 360 365
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
 370 375 380
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
 385 390 395 400
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
 405 410 415
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
 420 425 430
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
 435 440 445
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
 450 455 460
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
 465 470 475 480
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640

Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
 675 680 685
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
 690 695 700
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
 705 710 715 720
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
 725 730 735
 Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala
 740 745 750
 Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val
 755 760 765
 Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His
 770 775 780
 Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala
 785 790 795 800
 His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln
 805 810 815
 Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu
 820 825 830
 Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val
 835 840 845
 Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys
 850 855 860
 Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg
 865 870 875 880
 Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr
 885 890 895
 Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly
 900 905 910
 Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn
 915 920 925
 Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met
 930 935 940

Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg
 945 950 955 960

Thr Leu Glu Val Gln Ser Asp Tyr Ser Arg
 965 970

<210> 83
 <211> 3432
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Protein Lacking Motif A and Altered C-Terminus
 (ver.2); with Intron Y, Beta and 3

<400> 83
 atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
 gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120
 cgcggggacc cggcggtttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180
 gacgcacggc cgcctccccc cgccccctcc ttccgccagg tgggcctccc cggggtcggc 240
 gtccggtgtg ggttgagggc ggccgggggg aaccagcgac atgcggagag cagcgcaggc 300
 gactcagggc gcttcccccg caggtgtcct gcctgaagga gctggtggcc cgagtgtgc 360
 agaggctgtg cgagcgcggc gcgaagaacg tgctggcctt cggcttcgcg ctgctggacg 420
 gggcccgcg gggcccccgg gaggccttca ccaccagcgt gcgcagctac ctgccccaca 480
 cgggtgaccga cgcactgcgg gggagcgggg cgtgggggct gctgctgcgc cgcgtgggcg 540
 acgacgtgct ggttcacctg ctggcacgct gcgcgctctt tgtgctggtg gctcccagct 600
 gcgcctacca ggtgtgcggg ccgcgcgctgt accagctcgg cgtgccact caggcccggc 660
 ccccgccaca cgctagtga cccgaaggc gtctgggatg cgaacgggccc tggaaaccata 720
 gcgtcagga ggcgggggtc cccctgggccc tgcagcccc ggggtgcgagg aggcgcgggg 780
 gcagtgcag ccgaagtctg ccgttgccca agaggcccag gcgtggcgct gccctgagc 840
 cggagcggac gcccgttggg caggggtcct gggcccaccc gggcaggacg cgtggaccga 900
 gtgaccgtgg tttctgtgtg gtgtcacctg ccagaccgcg cgaagaagcc acctctttgg 960
 aggggtgcgt ctctggcacg cgcactccc acccatccgt gggccgccag caccacgcgg 1020
 gcccccatc cacatcgcg ccaccacgtc cctgggacac gccttgtccc ccggtgtacg 1080
 ccgagaccaa gcaattcctc tactcctcag gcgacaagga gcagctgcg ccctccttcc 1140
 tactcagctc tctgaggccc agcctgactg gcgctcggag gctcgtggag accatctttc 1200
 tgggttccag gccctggatg ccagggactc cccgcagggt gccccgcctg cccagcgct 1260
 actggcaaat gcggccccg tttctggagc tgcttgggaa ccacgcgcag tgcccctacg 1320
 ggggtgtcct caagacgcac tgcccgtgcg gagctgcgt caccacagca gccggtgtct 1380
 gtgcccggga gaagccccag ggctctgtgg cggcccccga ggaggaggac acagaccccc 1440
 gtcgcctggt gcagctgtc cgccagcaca gcagcccctg gcaggtgtac ggcttcgtgc 1500
 gggcctgcct gcgcgggctg gtgccccag gcctctgggg ctccaggcac aacgaacgcc 1560
 gcttcctcag gaacaccaag aagttcatct ccctgggga gcagtccaag ctctcgctgc 1620
 aggagctgac gtggaagatg agcgtgcggg actgcgctt gctgcgcagg agcccagggg 1680
 ttggtgtgtg tccggccgca gagcaccgtc tgctgagga gatcctggcc aagttcctgc 1740
 actggtgat gagtgttac gtgcgcgagc tgctcaggtc tttcttttat gtcacggaga 1800
 ccaggtttca aaagaacagg ctctttttct accggaagag tgtctggagc aagttgcaaa 1860
 gcattggaat cacagacac ttgaagaggg tgacagctgc ggagctgtcg gaagcagagg 1920
 tcaggcagca tcgggaagcc aggccgccc tgctgacgtc cagactccgc ttcaccccca 1980
 agcctgacgg gctgcggccg attgtgaaca tggactacgt cgtgggagcc agaacgttcc 2040
 gcagagaaaa gagggccgag cgtctcacct cgagggtgaa ggcactgttc agcgtgctca 2100
 actacgagcg ggcgcgcgcc cccggcctcc tgggcgcctc tgtgctgggc ctggacgata 2160
 tccacagggc ctggcgcacc ttcgtgctgc gtgtgcgggc ccaggacccg ccgcctgagc 2220
 tgtactttgt caaggacagg ctcacggagg tcatcgccag catcatcaaa cccagaaca 2280
 cgtactgcgt gcgtcggatg gccgtggtcc agaaggccgc ccatgggcac gtccgcaagg 2340

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ccttcaagag ccacgtctct accttgacag acctccagcc gtacatgcga cagttcgtgg 2400
ctcacctgca ggagaccagc ccgctgaggg atgccgtcgt catcgagcag agctcctccc 2460
tgaatgaggg cagcagtggc ctcttcgacg tcttcctacg cttcatgtgc caccacgccg 2520
tgcgcatcag gggcaagtcc tacgtccagt gccaggggat cccgcagggc tccatcctct 2580
ccacgctgct ctgcagcctg tgctacggcg acatggagaa caagctgttt gcggggattc 2640
ggcgggacgg gctgctcctg cgtttggtgg atgatttctt gttggtgaca cctcacctca 2700
cccacgcgaa aaccttcctc aggaccctgg tccgaggtgt ccctgagtat ggctgcgtgg 2760
tgaacttgcg gaagacagtg gtgaacttcc ctgtagaaga cgaggccctg ggtggcacgg 2820
cttttgttca gatgccggcc cacggcctat tcccctggtg cggcctgctg ctggataccc 2880
ggaccctgga ggtgcagagc gactactcca gctatgcccg gacctccatc agagccagtc 2940
tcaccttcaa ccgcggtctc aaggctggga ggaacatgcg tcgcaaactc tttggggctc 3000
tgcggtgtaa gtgtcacagc ctgtttctgg atttgcaggt gaacagcctc cagacggtgt 3060
gcaccaacat ctacaagatc ctctgctgc aggcgtacag gtttcacgca tgtgtgctgc 3120
agctccatt tcatacagaa gtttggaaga accccacatt tttcctgcgc gtcatctctg 3180
acacggcctc cctctgctac tccatcctga aagccaagaa cgcagccgaa gaaaacattt 3240
ctgtcgtgac tcttgcggtg cttgggtcgg gacagccaga gatggagcca cccgcagac 3300
cgtcgggtgt ggcagcgtt cgggtgtctc ctgggagggg agttgggctg ggcctgtgac 3360
tcctcagcct ctgttttccc ccagggatgt cgctgggggc caagggcgcc gccggccctc 3420
tgccctccga ga 3432

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<210> 84
 <211> 1122
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Protein Lacking Motif A and Altered C-Terminus
 (ver.2); encoded by SEQ ID NO:83 with Intron Y
 ORF1

<400> 84
 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
 1 5 10 15
 His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
 65 70 75 80
 Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
 85 90 95
 Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
 100 105 110
 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
 115 120 125
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
 130 135 140

Pro	Pro	Glu	Ala	Phe	Thr	Thr	Ser	Val	Arg	Ser	Tyr	Leu	Pro	Asn	Thr	145	150	155	160
Val	Thr	Asp	Ala	Leu	Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu	Leu	Arg	165	170	175	
Arg	Val	Gly	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu	180	185	190	
Phe	Val	Leu	Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro	195	200	205	
Leu	Tyr	Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala	210	215	220	
Ser	Gly	Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser	225	230	235	240
Val	Arg	Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg	245	250	255	
Arg	Arg	Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro	260	265	270	
Arg	Arg	Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly	275	280	285	
Ser	Trp	Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe	290	295	300	
Cys	Val	Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu	305	310	315	320
Gly	Ala	Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln	325	330	335	
His	His	Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp	340	345	350	
Thr	Pro	Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser	355	360	365	
Ser	Gly	Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu	370	375	380	
Arg	Pro	Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu	385	390	395	400
Gly	Ser	Arg	Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu	405	410	415	
Pro	Gln	Arg	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly	420	425	430	
Asn	His	Ala	Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro	435	440	445	

Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
 450 455 460
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
 465 470 475 480
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
 675 680 685
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
 690 695 700
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
 705 710 715 720
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
 725 730 735
 Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala
 740 745 750

Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val
 755 760 765
 Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His
 770 775 780
 Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala
 785 790 795 800
 His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln
 805 810 815
 Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu
 820 825 830
 Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val
 835 840 845
 Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys
 850 855 860
 Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg
 865 870 875 880
 Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr
 885 890 895
 Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly
 900 905 910
 Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn
 915 920 925
 Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met
 930 935 940
 Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg
 945 950 955 960
 Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile
 965 970 975
 Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met
 980 985 990
 Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe
 995 1000 1005
 Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr
 1010 1015 1020
 Lys Ile Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln
 1025 1030 1035 1040
 Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg
 1045 1050 1055

Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys
 1060 1065 1070

Asn Ala Glu Glu Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly
 1075 1080 1085

Ser Gly Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly
 1090 1095 1100

Ser Phe Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu Phe Ile
 1105 1110 1115 1120

Gly Ala

<210> 85
 <211> 1037
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Protein Lacking Motif A and Altered C-Terminus
 (ver.2); encoded by SEQ ID NO:83 with Intron Y
 ORF2 after the termination codon

<400> 85
 Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
 1 5 10 15

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg
 20 25 30

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
 35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
 50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
 65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
 85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
 100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
 115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg
 130 135 140

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 Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
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(ver.2); encoded by SEQ ID NO:83 with Intron Y
ORF3

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<211> 8
<212> PRT
<213> Homo sapiens

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<400> 90
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  1             5

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<210> 91
<211> 8
<212> PRT
<213> Unknown

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<220>
<223> Description of Unknown Organism: Consensus P-loop
      Motif Sequence found in large number of protein
      families

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<221> MOD_RES
<222> (2)..(5)
<223> Wherein Xaa is any residue

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<400> 91
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<210> 92
<211> 17
<212> PRT
<213> Homo sapiens

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<400> 92
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  1             5             10             15

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Gly

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<210> 93
<211> 9
<212> PRT
<213> Unknown

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<220>
 <223> Description of Unknown Organism: Consensus c-Alb
 SH3 binding peptide

<220>
 <221> MOD_RES
 <222> (2)..(5)
 <223> Wherein Xaa is any residue

<220>
 <221> MOD_RES
 <222> (7)..(8)
 <223> Wherein Xaa is any residue

<400> 93
 Pro Xaa Xaa Xaa Xaa Pro Xaa Xaa Pro
 1 5

<210> 94
 <211> 17
 <212> PRT
 <213> Homo sapiens

<400> 94
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Pro

<210> 95
 <211> 14
 <212> DNA
 <213> Unknown

<220>
 <223> Description of Unknown Organism: General Target
 Sequence Recognized by Hairpin Ribozyme

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 <221> modified_base
 <222> (1)..(3)
 <223> Wherein N is G, U, C or A

<220>
 <221> modified_base
 <222> (5)
 <223> Wherein N is G, U, C or A

<220>
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 <222> (9)..(14)
 <223> Wherein N is G, U, C or A

<400> 95
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 <210> 96
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Amplification
 Primer Design Based on EST Sequence GenBank
 Accession Number AA281296

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 <210> 97
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Amplification
 Primer Design Based on EST Sequence GenBank
 Accession Number AA281296

 <400> 97
 tccacgcgtc ctgcccggt g 21

 <210> 98
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Amplification
 Primer Design Based on EST Sequence GenBank
 Accession Number AA281296

 <400> 98
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 <210> 99
 <211> 48
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Amplification
 Primer Design Based on EST Sequence GenBank
 Accession Number AA281296

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 <210> 100
 <211> 20

<212> DNA
 <213> Artificial Sequence

<220>
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 GenBank Accession Number AA281296

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 GenBank Accession Number AA281296

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<210> 102
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<220>
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<210> 104
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<220>
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Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

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<210> 105
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<212> DNA
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<220>
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GenBank Accession Number AA281296

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<210> 106
<211> 24
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<210> 107
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<210> 116
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 GenBank Accession Number AA281296

<400> 124
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 GenBank Accession Number AA281296

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<210> 126
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<210> 135
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<223> Description of Artificial Sequence: Synthesized
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GenBank Accession Number AA281296

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<210> 136

<211> 19

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

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<211> 21

<212> DNA

<213> Artificial Sequence

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GenBank Accession Number AA281296

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<210> 138

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<212> DNA

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<223> Description of Artificial Sequence: Synthesized
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GenBank Accession Number AA281296

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<212> DNA

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<223> Description of Artificial Sequence: Synthesized
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GenBank Accession Number AA281296

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<210> 140
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GenBank Accession Number AA281296

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GenBank Accession Number AA281296

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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
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GenBank Accession Number AA281296

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ggc 63

<210> 143
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<212> DNA
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GenBank Accession Number AA281296

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 GenBank Accession Number AA281296

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 gagccgagtc ctg 73

<210> 145
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthesized
 Amplification Primer Design based on EST Sequence
 GenBank Accession Number AA281296

<400> 145
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<210> 146
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 <212> DNA
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<220>
 <223> Description of Artificial Sequence: Synthesized
 Amplification Primer Design based on EST Sequence
 GenBank Accession Number AA281296

<400> 146
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<210> 147
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 Amplification Primer Design based on EST Sequence
 GenBank Accession Number AA281296

<400> 147
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<210> 148
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 148

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26

<210> 149

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 149

gcggatccgt tcagatgccg gcccac

26

<210> 150

<211> 9

<212> PRT

<213> Homo sapiens

<400> 150

Pro Glu Met Glu Pro Pro Arg Arg Pro
1 5

<210> 151

<211> 4

<212> PRT

<213> Homo sapiens

<400> 151

Ala Ala Glu His
1

<210> 152

<211> 6

<212> PRT

<213> Homo sapiens

<400> 152

Val Gln Met Pro Ala His
1 5

<210> 153

<211> 5

<212> PRT

<213> Homo sapiens

<400> 153
Val Gly Leu Gly Leu
1 5

<210> 154
<211> 4
<212> PRT
<213> Homo sapiens

<400> 154
Arg Ala Thr Ser
1

<210> 155
<211> 622
<212> PRT
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<220>
<223> N-Terminal Truncated Telomerase (ver.2); encoded
by SEQ ID NO:51, with Y Intron ORF3

<400> 155
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15
His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30
Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45
Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60
Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
65 70 75 80
Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu
85 90 95
Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys
100 105 110
Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
115 120 125
Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
130 135 140
Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
145 150 155 160
Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg

165							170							175		
Arg	Val	Gly	Asp 180	Asp	Val	Leu	Val	His 185	Leu	Leu	Ala	Arg	Cys 190	Ala	Leu	
Phe	Val	Leu 195	Val	Ala	Pro	Ser	Cys 200	Ala	Tyr	Gln	Val	Cys 205	Gly	Pro	Pro	
Leu	Tyr 210	Gln	Leu	Gly	Ala	Ala 215	Thr	Gln	Ala	Arg	Pro 220	Pro	Pro	His	Ala	
Ser 225	Gly	Pro	Arg	Arg	Arg 230	Leu	Gly	Cys	Glu	Arg 235	Ala	Trp	Asn	His	Ser 240	
Val	Arg	Glu	Ala	Gly 245	Val	Pro	Leu	Gly	Leu 250	Pro	Ala	Pro	Gly	Ala 255	Arg	
Arg	Arg	Gly	Gly 260	Ser	Ala	Ser	Arg	Ser 265	Leu	Pro	Leu	Pro	Lys 270	Arg	Pro	
Arg	Arg	Gly 275	Ala	Ala	Pro	Glu	Pro 280	Glu	Arg	Thr	Pro	Val 285	Gly	Gln	Gly	
Ser 290	Trp	Ala	His	Pro	Gly	Arg 295	Thr	Arg	Gly	Pro	Ser 300	Asp	Arg	Gly	Phe	
Cys 305	Val	Val	Ser	Pro	Ala 310	Arg	Pro	Ala	Glu	Glu 315	Ala	Thr	Ser	Leu	Glu 320	
Gly	Ala	Leu	Ser	Gly 325	Thr	Arg	His	Ser	His 330	Pro	Ser	Val	Gly	Arg 335	Gln	
His	His	Ala	Gly 340	Pro	Pro	Ser	Thr	Ser 345	Arg	Pro	Pro	Arg	Pro 350	Trp	Asp	
Thr	Pro	Cys 355	Pro	Pro	Val	Tyr	Ala 360	Glu	Thr	Lys	His	Phe 365	Leu	Tyr	Ser	
Ser 370	Gly	Asp	Lys	Glu	Gln	Leu 375	Arg	Pro	Ser	Phe	Leu 380	Leu	Ser	Ser	Leu	
Arg 385	Pro	Ser	Leu	Thr	Gly 390	Ala	Arg	Arg	Leu	Val 395	Glu	Thr	Ile	Phe	Leu 400	
Gly	Ser	Arg	Pro	Trp 405	Met	Pro	Gly	Thr	Pro 410	Arg	Arg	Leu	Pro	Arg 415	Leu	
Pro	Gln	Arg	Tyr 420	Trp	Gln	Met	Arg	Pro 425	Leu	Phe	Leu	Glu	Leu 430	Leu	Gly	
Asn	His	Ala 435	Gln	Cys	Pro	Tyr	Gly 440	Val	Leu	Leu	Lys	Thr 445	His	Cys	Pro	
Leu	Arg 450	Ala	Ala	Val	Thr	Pro 455	Ala	Ala	Gly	Val	Cys 460	Ala	Arg	Glu	Lys	
Pro	Gln	Gly	Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg	

465 470 475 480
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly
 610 615 620

2 / concave